



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 190795

TO: Ruixiang Li
Location: rem/4D59/4C70
Art Unit: 1646
Wednesday, May 31, 2006
Case Serial Number: 10/619992

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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78733

190795

M9

STIC-Biotech/ChemLib

From: Li, Ruixiang
Sent: Tuesday, May 23, 2006 9:19 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/619,992

Please do a standard search on:

SEQ ID NO: 2 against interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D59
Mail Box 4C70
(571) 272-0875

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: May 24, 2006, 12:48:33 ; Search time 35 Seconds
 (Without alignments)
 2978.542 Million cell updates/sec

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

- 1: Issued_Patents_AA,*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/R_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1/2/iaa/backfiles1/2/iaa

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-09-921-099A-2
 Sequence 2, Application US/09921099A
 ; Patent No. 6602707

; GENERAL INFORMATION:

; APPLICANT: Hefenreider, Steven
 ; APPLICANT: Merkins, Louise
 ; APPLICANT: Bennett, Robert
 ; APPLICANT: Seiss, Donald
 ; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene and Current Application Number: US/09/921,099A
 ; CURRENT FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1191
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-921-099A-2

Query Match 100.0%; Score 6215; DB 2; Length 1191;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Gaps 0;
 Spans 0; Indels 0;

Qy |||||||1MIVQAAQWTERFLSPCIPYNEFEDENVTKPISLGCSHTVKCTCLNKLKACCPDQTAINTD 60
 Db 1 MIVQAAQWTERFLSPCIPYNEFEDENVTKPISLGCSHTVKCTCLNKLKACCPDQTAINTD 60

Qy |||||||2IDVLPLNFALLQVQPHQSIKSLNLGNNKHYEAKKVEDIALYLKPUSGGKWA 120
 Db 61 IDVLPLNFALLQVQPHQSIKSLNLGNNKHYEAKKVEDIALYLKPUSGGKWA 120

Qy |||||||3LNQSAISRPMKQLVTLVNCOLVVEGGRVRAMARASLGERTVTEILQHQNPQLSANL 180
 Db 61 IDVLPLNFALLQVQPHQSIKSLNLGNNKHYEAKKVEDIALYLKPUSGGKWA 120

Qy |||||||4LNQSAISRPMKQLVTLVNCOLVVEGGRVRAMARASLGERTVTEILQHQNPQLSANL 180
 Db 121 LNQSAISRPMKQLVTLVNCOLVVEGGRVRAMARASLGERTVTEILQHQNPQLSANL 180

Qy |||||||5WAARVARGCQFLGPAMOBEALKLVLLALEDGSALSRLKVVLVFWVORLEPREPQASKTSIG 240
 Db 181 WAARVARGCQFLGPAMOBEALKLVLLALEDGSALSRLKVVLVFWVORLEPREPQASKTSIG 240

Qy |||||||6RIVVOLYRASPFKVKTRKEDDSIMOLKEEFSYEALRERHDAQIVTIAIMEAGLRISPEQW 300
 Db 241 HVVQQLYRASPFKVKTRKEDDSIMOLKEEFSYEALRERHDAQIVTIAIMEAGLRISPEQW 300

Qy |||||||7SSLYGLPLAHSHMSODIKLQSPESFAKSYQELTIVLQRTGDPAHLNRSPHELEANI 360
 Db 301 SSLYGLPLAHSHMSODIKLQSPESFAKSYQELTIVLQRTGDPAHLNRSPHELEANI 360

Qy |||||||8SSLYGLPLAHSHMSODIKLQSPESFAKSYQELTIVLQRTGDPAHLNRSPHELEANI 360

QY 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-921-09A-4

QY 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420
; Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
; Matches 1190; Conservative 0;

QY 421 QGGCPRGTCNTFAHSOEBELEYRLRKINKINATVRTPPLANKVGNNTVTAGNIVSI 480
; Query Match 99.9%; Score 6207; DB 2; Length 1191;
; 421 QGGCPRGTCNTFAHSOEBELEYRLRKINKINATVRTPPLANKVGNNTVTAGNIVSI 480
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 481 GSTETGCKIVSTNGISNAENSVSQIISRSTDSTALETWVKVGKVGANGONAGPSAD 540
; 481 GSTETGCKIVSTNGISNAENSVSQIISRSTDSTALETWVKVGKVGANGONAGPSAD 540
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTEINSVQKSSFLTRPVYPHSENQFQ 600
; 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTEINSVQKSSFLTRPVYPHSENQFQ 600
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 601 DPTQIPFEVPOYQYPPPTVAGVACPVPRVSRNNVPESSLPPASMPYDHYST 660
; 601 DPTQIPFEVPOYQYPPPTVAGVACPVPRVSRNNVPESSLPPASMPYDHYST 660
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 661 FSPDRMNSSPQPQQPQPYGVPPVPGMATAVYSSRIRRPMQDDIRNSLPPM 720
; 661 FSPDRMNSSPQPQQPQPYGVPPVPGMATAVYSSRIRRPMQDDIRNSLPPM 720
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 721 DMHSSYQTSLRERTNSLDGYSVACQPSRPTVPLPRBCGHILKTSCEQIRKPD 780
; 721 DMHSSYQTSLRERTNSLDGYSVACQPSRPTVPLPRBCGHILKTSCEQIRKPD 780
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 781 QWAQYHTQAKPLVSSTLPVATOSOPTPSPLSVFDRADSESSVSGKTFEEDELSHYSPPWS 840
; 781 QWAQYHTQAKPLVSSTLPVATOSOPTPSPLSVFDRADSESSVSGKTFEEDELSHYSPPWS 840
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 841 CGTIGSCINAIDSEPKDVTANSNAVLMDSDQDKRVRVHLFETORRKEDDEPIPDSGP 900
; 841 CGTIGSCINAIDSEPKDVTANSNAVLMDSDQDKRVRVHLFETORRKEDDEPIPDSGP 900
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

QY 901 ISKWMGAISSRSRTGHTDPQATASQGSAKTPISVSYNAVDRNSYBEATS 960
; 901 ISKWMGAISSRSRTGHTDPQATASQGSAKTPISVSYNAVDRNSYBEATS 960
; DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

Db 901 ISKWMGAISSRSRTGHTDPQATASQGSAKTPISVSYNAVDRNSYBEATS 960
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-921-09A-4

Db 960 1 MVQAOAWTERLSCPCYCNEFENDTHKPIISGCSHTVCKTCILKHKACPFQDQTAINTD 60
; 1 MVQAOAWTERLSCPCYCNEFENDTHKPIISGCSHTVCKTCILKHKACPFQDQTAINTD 60
; IDVLVPNFFALLQVGAQVDPHQSIKUSNLGENKHVEAKKVEDIALYLAKPLSGGGWS 120
; IDVLVPNFFALLQVGAQVDPHQSIKUSNLGENKHVEAKKVEDIALYLAKPLSGGGWS 120

Db 600 1 MAVQAQWTEELSCPCYCNEFENDTHKPIISGCSHTVCKTCILKHKACPFQDQTAINTD 60
; 1 MAVQAQWTEELSCPCYCNEFENDTHKPIISGCSHTVCKTCILKHKACPFQDQTAINTD 60

Db 660 1 LNQALSRRPMQRKLVNLNCOLVVEERGRVRAMRAARSLGERTVTELILQHONPOOLSANL 180
; 1 LNQALSRRPMQRKLVNLNCOLVVEERGRVRAMRAARSLGERTVTELILQHONPOOLSANL 180

Db 720 1 WAAVRARGCQFLGPMQEAALKLVIALEDASLASKVLFVWORLEPRPQASKSIG 240
; 1 WAAVRARGCQFLGPMQEAALKLVIALEDASLASKVLFVWORLEPRPQASKSIG 240

Db 780 1 181 WAAVRARGCQFLGPMQEAALKLVIALEDASLASKVLFVWORLEPRPQASKSIG 240
; 1 181 WAAVRARGCQFLGPMQEAALKLVIALEDASLASKVLFVWORLEPRPQASKSIG 240

Db 840 1 241 HVVQLJRAASCFKVTKRDEDSLMOKEFRSYEARREHDQIVMIAMEGLRISPEQW 300
; 1 241 HVVQLJRAASCFKVTKRDEDSLMOKEFRSYEARREHDQIVMIAMEGLRISPEQW 300

Db 900 1 241 HVVQLJRAASCFKVTKRDEDSLMOKEFRSYEARREHDQIVMIAMEGLRISPEQW 300
; 1 241 HVVQLJRAASCFKVTKRDEDSLMOKEFRSYEARREHDQIVMIAMEGLRISPEQW 300

Db 960 1 301 SSLLYGDLAHKSHMOSITIKLUQSPESPAKSQVBLTTLVQRTGDPANLNURPHILEANI 360
; 1 301 SSLLYGDLAHKSHMOSITIKLUQSPESPAKSQVBLTTLVQRTGDPANLNURPHILEANI 360

Db 360 1 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420
; 1 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

Db 420 1 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420
; 1 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

Db 480 1 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420
; 1 361 DPNPDAVSPWQOLENAWAVKTWVAGLVDIPIQNSRKGHETPQOPNSKIKTSMQRDLR 420

Db 540 1 421 QGGCPRGTCNTFAHSOEBELEYRLRKINKINATVRTPPLANKVGNNTVTAGNIVSI 480
; 1 421 QGGCPRGTCNTFAHSOEBELEYRLRKINKINATVRTPPLANKVGNNTVTAGNIVSI 480

Db 600 1 421 QGGCPRGTCNTFAHSOEBELEYRLRKINKINATVRTPPLANKVGNNTVTAGNIVSI 480
; 1 421 QGGCPRGTCNTFAHSOEBELEYRLRKINKINATVRTPPLANKVGNNTVTAGNIVSI 480

Db 660 1 481 GSTETGCKIVSTNGISNAENSVSQIISRSTDSTALETWVKVGKVGANGONAGPSAD 540
; 1 481 GSTETGCKIVSTNGISNAENSVSQIISRSTDSTALETWVKVGKVGANGONAGPSAD 540

Db 720 1 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTEINSVQKSSFLTRPVYPHSENQFQ 600
; 1 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTEINSVQKSSFLTRPVYPHSENQFQ 600

Db 780 1 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTEINSVQKSSFLTRPVYPHSENQFQ 600
; 1 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTEINSVQKSSFLTRPVYPHSENQFQ 600

Db 840 1 601 DPTQIPFEVPOYQYPPPTVAGVACPVPRVSRNNVPESSLPPASMPYDHYST 660
; 1 601 DPTQIPFEVPOYQYPPPTVAGVACPVPRVSRNNVPESSLPPASMPYDHYST 660

Db 900 1 661 FSPDRMNSSPQPQQPQPYGVPPVPGMATAVYSSRIRRPMQDDIRNSLPPM 720
; 1 661 FSPDRMNSSPQPQQPQPYGVPPVPGMATAVYSSRIRRPMQDDIRNSLPPM 720

Db 960 1 721 DMHSSYQTSLRERTNSLDGYSVACQPSRPTVPLPRBCGHILKTSCEQIRKPD 780
; 1 721 DMHSSYQTSLRERTNSLDGYSVACQPSRPTVPLPRBCGHILKTSCEQIRKPD 780

Db 1020 1 781 QWAQYHTQAKPLVSSTLPVATOSOPTPSPLSVFDRADSESSVSGKTFEEDELSHYSPPWS 840
; 1 781 QWAQYHTQAKPLVSSTLPVATOSOPTPSPLSVFDRADSESSVSGKTFEEDELSHYSPPWS 840

Db 1080 1 841 CGTIGSCINAIDSEPKDVTANSNAVLMDSDQDKRVRVHLFETORRKEDDEPIPDSGP 900
; 1 841 CGTIGSCINAIDSEPKDVTANSNAVLMDSDQDKRVRVHLFETORRKEDDEPIPDSGP 900

Db 1080 1 901 ISKWMGAISSRSRTGHTDPQATASQGSAKTPISVSYNAVDRNSYBEATS 960
; 1 901 ISKWMGAISSRSRTGHTDPQATASQGSAKTPISVSYNAVDRNSYBEATS 960

Db 1140 1 960 ISKWMGAISSRSRTGHTDPQATASQGSAKTPISVSYNAVDRNSYBEATS 960
; 1 960 ISKWMGAISSRSRTGHTDPQATASQGSAKTPISVSYNAVDRNSYBEATS 960

Db 1141 1 1141 SQQPLVPSISNASCLPITSVSAGNLILKTHVASEDKDFLKPVANGKVN 1191
; 1 1141 SQQPLVPSISNASCLPITSVSAGNLILKTHVASEDKDFLKPVANGKVN 1191

Db 1141 1 1141 SQQPLVPSISNASCLPITSVSAGNLILKTHVASEDKDFLKPVANGKVN 1191
; 1 1141 SQQPLVPSISNASCLPITSVSAGNLILKTHVASEDKDFLKPVANGKVN 1191

RESULT 2
; Sequence 4, Application US-09921099A
; Patent No. 6622707
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921, 099A
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4

QY 961 SAVYVERDRFTVUTSGHRKHSSTGDLISLEIQAQNSNLIGOREANALAMQOKNSLDE 1020
Db 961 SHYVERDRFTVUTDLSGHRKHSSTGDLISLEIQAQNSNLIGOREANALAMQOKNSLDE 1020
QY 1021 GRHLTNILSSEHIELNGELOSSDYTDATPKPDRTELELSALDTDEPDCOSEPEEIL 1080
Db 1021 GRHLTNILSSEHIELNGELOSSDYTDATPKPDRTELELSALDTDEPDCOSEPEEIL 1080
QY 1081 DLQLGSSONDOLLINGNAVENSHIPVQOHQKEPPKKQSLGDHDWILBQKTIPLPTSCF 1140
Db 1081 DLQLGSSONDOLLINGNAVENSHIPVQOHQKEPPKKQSLGDHDWILBQKTIPLPTSCF 1140
QY 1141 SQPLPVISNASCCLPITTSVSAIGNLIKIHVNSEDKNDFLKEVANGKVN 1191
Db 1141 SQPLPVISNASCCLPITTSVSAIGNLIKIHVNSEDKNDFLKEVANGKVN 1191

RESULT 3
US-09-921-099A-11
; Sequence 11, Application US/09921099A
; Patent No. 6502707
; GENERAL INFORMATION:
; APPLICANT: Hefenesider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921,099A
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-921-099A-11

Query Match 13.6%; Score 843; DB 2; Length 1048;
Best Local Similarity 30.6%; Pred. No. 4.3e-59;
Matches 238; Conservative 99; Mismatches 278; Indels 162; Gaps 23;

QY 4 QKAQWTEFLSPICYNEFPDENWKHPISLGCSHTVKTCICLKHAR--KACPDDQTAINTDI 61
Db 6 OGGQWQEVLCSSICNRHFNE TFLPSLICHGIVCKCAERENQTKPCPHDKWTHSP 64
QY 62 DVLUPVNPFALLQDVGAGQVDPDHOSIKSLNGLGENRHYEAKKCYEDFLAYLKPLGGKVASL 121
Db 65 SEYPNNVALLSVI--FPRKQMTLSGAVEAKRVDOLSIQ-IAKFREADSERG-GTV 119
QY 122 NOSALSRPMQRKLVTLVNCOLQVLEEGVRAMARSILGERTVTELLQHQMQQQLSANW 181
Db 120 SREETSLTORKVALLCYQHEDVGRKLTKMCRGISERVNTIEILSISONTHVSOLW 179
QY 182 AAVRARGCQFLGPAMOBEALKVUILLAEDGSALSRSKVLVLFVORLPRFPOASKTSIGH 241
Db 180 SAVRANGCQFGPAMQDDVLILMLTETGCIARKLQMVQTLASDVPQSKVUGH 239
QY 242 VVOLLYRASCFRKVTKBEDSSIMOLKEKEFRSYEARREHDQIAVHAMEACIRISBOWS 301
Db 240 VVOLLYRASCENVLRKGESSIMOLKEKEFRYTESRKEHDSQIVQAFESGRIGDOWS 299
QY 302 SLYLGDLAKHSMQSTIDKUQSPESAKVSKVLTWLQRTGDPN-----LNRIP 352
Db 300 ALLYADOSHRSRHMOSTIDKLOSKNSYOOQVBELRL---AGSOTMSLUPPAYRYFLQVIP 356
QY 353 HELLANIIDPNPDAVSPTEQLENAMVAKTVVHGLUDFIQY--SRKGHETPQPQNS 409
Db 357 CLEFFAGIEHEDTSMSMIGDALHOIRILK--LHCSDODLREKMPKEERRSYLQLQAVPGG 414
QY 410 KXKTSMDRLROQGCPGRTGNTFAHSQEBELKYRUNKKINATVRTPLINKVGVNTV 469
Db 415 --MGGPGGSG-----GAFAIRI----- 430

QY 470 TTAGNUVISVIGSTETGKVPUSTNGISNAENSVSOLISRSTDSTLRALETVKVKGVA 529
Db 431 ---GLHPLYSQDENGERSRSRTNPKNDSNSPQ----- 461
QY 530 NGQNAAGPSADSVTENKGSRKPTPSVNAATSAGSNSVNGTEBLNSVQKSSPFLTRVY 589
Db 462 -----TPPKQPKQKRYQMGIPENRMG----YSSDAPPFISHQQ 497
QY 590 PPHESENQYFOPRTOIPFEVPOYPOGYYRPPTVPGAVAPCVPRFVRSNNVPESSLPP 649
Db 498 PPP---OFFNS---QHLPQRFRGGRGAPPPPQP-----MPLIGD----MPG 539
QY 650 ASMPYADHYSPTSPPRMNSP----YQPQQPQYGPVPPVPSGMYAPVUDSRRIWRRP 704
Db 540 APMMQATEVLT-ADGQMVNGPQRVYIMQSPTHLPQGPVWMPQQMVPPQSMTPVGGP 598
QY 705 MYQDDIRNSLSPMDVMHSS-VOTSURRNSLDGYYV--ACQPBEPRTV 757
Db 599 M-----GPWGPMTSIPVQVQVPPNMTATSPGSVYPAASPGQOPHTI 643

RESULT 4
US-10-104-047-3665
; Sequence 3665, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIORITY FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3665
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-3665

Query Match 9.8%; Score 611; DB 2; Length 522;
Best Local Similarity 34.1%; Pred. No. 1e-40;
Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

QY 618 YPPPPPPVAGVAPCVPRFVRSNNVVESSUPSPASMYADHYSPTSPPRMNSPQYOPPP 677
Db 2 YYTPPP-----QCYSRFRV---PPPSAPEPAPPYLHDHPPYL-QERVINSQGTQPO 49
QY 678 OPYGPVPPVPSGMAMYAVPSRSRIWRPPMQRDDIIRSNLSPMPDVHSV--YQTSLER 735
Db 50 Q-----YPP-----YPSHYDGRGRVYVAPSYTREEIFRESPI-PIEIPPAAVPSYPSRER 100
QY 736 YNSLDGYSSVACQP----PS---ERTRFLPRLPRECGHLKTSCEBQIRRKPDQWQHT 787
Db 101 YQIESVYVPAHPTOIRPSLREPPSYLPPQP---HPSLDBLRRKEIMQLE 156
QY 788 QKAPLYSTSLLVATOSPPSPFLSFVDFRADFSESVSGTKFEEDHSHYSPWSGCTGSC 847
Db 157 RK---VISPPPA-PSPLTP-PTFHPEEFLDEDLKJAG-KIKGNDYQSYPWSDCTIGS 210
QY 848 INADSEPKDVTANSVAVLMDSGVYKRRMHLFETORTKE--EPIIIPSDGPIISKW 905
Db 211 IGTKDAPKDVAGSVEMMINVESKGW--RDORLQRRRAETSDDDLIPFGDRPTVSR 268
QY 906 GAISRSRTGHTDVOATASQSAKTPISVSDVYVNAVDSRW-SSYG--NEATSS 961
Db 269 GAISRSRTGHTDVOATASQSAKTPISVSDVYVNAVDSRW-SSYG--GTHGGWGAQPSYHONIPSQ 326
QY 962 AHYVERDRFTVUTDLSGHRK-HSSTGDLISLBLOQ-----AKNSILLR 1004
Db 327 GHFSERERISMSEVASHGKPLPSABEREQLLELQNLHQI-SQQTQULRGPEAVSNRLVLR 386

Qy 1005 EANALAMOO-----KWNLSDEGRHLTLNL--LSKEIELRNGELQSODYTEDATDKPD 1054
Db 387 EANTILAGQSOPPPPPPWPWMISRSQSLBHQVEREIGRKTRLEMSME-NQCSLDM-- 443
Qy 1055 RDIIELELSALDDE--PDGSEPIEELDOLGIISQNODLNGAVENGHPVQHQKEP 1112
Db 444 -----SKUNTSKQANGQPEPQNKV-----PAEDLTTFSDVPNGSALTQBNISL 488
Qy 1113 PKQKKSLSL 1120
Db 489 LSNKTSLL 496

RESULT 5

; Sequence 36, Application US/09854856

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Donoho, Erin
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854, 856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206, 015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 2185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1) .. (2185)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-854-856-36

Query Match 3.1%; Score 194; DB 2; Length 2185;
Best Local Similarity 18.5%; Pred. No. 1e-05; Mismatches 506; Index 362; Gaps 49;

Matches 235; Conservative 167; Mismatches 506; Index 362; Gaps 49;

Qy 48 KKCPCPDATINT-----DIDVIPVNFAOLLOWGAQPDHOSIKLNSLNGEN 92
Db 315 KREASFANSVIGPEMAPEMPEEKYDVSVDVYAFGMCMLENATSETP----- 361
Qy 93 KHYEVAKKCVEDIALYVPLSLGGKGVASLNGASL-----SRPMORKLYLVN 139
Db 362 -----YSECQNAQIYKRVTSQVK-PASFDKVAIPEKEIEGCCIRONKDERYSIKDLN 415
Qy 140 COLVEEFGVRAMAARSIGERTVTETLQHONPQOLSANIAVARGCQLFLGPMQEE 199
Db 416 HAFQEETGVRLAEBDGEKIKAJWLWTRBDIKKL-----GYKDNE 460
Qy 200 ALKVLVLALEDGSALSRKVLFVFLVORLEPRPQASKTSIGHVQLYRASCFFKVTKRDE 259
Db 461 AIEF-----SFDLERDVPUEDAQVQENVEGVCEDGHKTMKAIKDR-- 501

Qy 260 DSIMLQIKEKEFYSYEALRREHDAQIVHTAMEAGLRISPEQWSLLYGDLAHKSHMOSIID 319
Db 502 - VSLIKKREOR - QLVREOESKK-----KOEESSLKQVEOESSASQTCGK 544
Qy 320 KQPSPEFAKSTSOELTIVLQRGDP-----ANURLRPYLELLANIIDPDAVSPTW 371
Db 545 QLPSSASTGPTAATTSASVSTQVEPEEPADQHQOLQYQCPISVLS-DGTVDGCGSS 602
Qy 372 EQLENAMAVKTVVHGLUDPFIQNSRKCHET-----POQPNSKXKTMCRDL 419
Db 603 VFTESRVSSQTVSYG-----SQHBOAHSTGTVPHGHPSTVQAQSPHGVVPPSSVAQG 656

RESULT 6

US-10-010-720-36

; Sequence 36, Application US/10010720

; GENERAL INFORMATION:
; Patent No. 6858419
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Genn
; APPLICANT: BeltrandeLrio, Hector

Qy 420 ROOGCCPREGNTCAHSQEEBLEKYLRLNNKINATVRTFPLANKVGNNTVTTAGNVISV 479
Db 657 OSQGQ-PSSSLTGTGSSSQIIOHQ-----QQQIQQTAPQ----- 692
Qy 480 IGSTETGKIVUPSTGNGISNENSQOLISRSTDSTLRALETVKVGKVANGQNAAGPSA 539
Db 693 -----QTVQYLSQ-TSISSEAT-----TAQPVISQPA 719
Qy 540 DSVTENKIGAPPKTPVSNAATSAQPSN--VGTEUNSVQKSSPFLTRV-----PVYPP 591
Db 720 POFVL-QVSACKQLPVSQPYTICERPOVPAQSVVPPHTISGALIFLPVQQLPPTBLP- 777

Qy 592 HSENIOYFQDPRTOIPFEVPOY--POTGYPPPTVPGVAPCVRFPVRSNNVPESSL- 648
Db 778 -----QFVFSQIPISTPVHSTAOTGFSSLPTMAIGITQ-PLTIAASSATTAI PG 827

Qy 649 -----PASMPYADHSTSFRDRMNSPPY---QZPP-----PQPKGPVPPVSGMVAPV 694
Db 828 VSTVUVSQLP-----TILLQPTQLPSQVHPOLLQPAVQSMGIPANLGQAAEVPLSGDVL 882

Qy 695 YDSRRFWRPPMQRDIRRSNLSLPPMDVMMSSVYQSLRERYNSLDGYSVACQCPSE PR 754
Db 883 YQGPFRPLPPOYGPSENIAFPSSNVAVCINITVLAQPMPTBLATGQFPTVQPVNE 942

Qy 755 RTVPL-----PREPGH-----KTCSEBQIRRKPDQWQYHTOKAPLUSSTLPAQ 802
Db 943 LLVPMGEGVQGVQSVQPGSGLAQAPITSQDAVLES-----TQGVQVAPAEVVA 994

Qy 803 SP--TPSPPL-FSVDF-----RADFSEKSVGTRKFEEDHLSHVSPWSCCTIGSCINAI 851
Db 995 QPQATOPIITLASSVDSAHSDVASHGMDGENEVUPSSGRHECRTKRMKRSVRSRHEK 1054

Qy 852 DSEPKOVIAN-----SNAVLMUDGSDVKAQKRVHLETORIETRKEEPPIIPSDGPIISKWG 906
Db 1055 TSRPKURILANNSKGDRVVECOLETINRKWMTFKFOLGDNPPEEATIMWANDFL--- 1110

Qy 907 AISRSS-----RTGYHTTDPPVQA-----TASQ-----GSATKP 934
Db 1111 AIERESPVDQVRELEKADEMLSEDVSVEPEKGDDQGLESLOCKDDYGFSGSOKLEGEFKQ 1170

Qy 935 ISVSDVYVYYNAVDSERWSYSNEATSAAHYERDRFTVTDLSGHRIKS---TGDLI-SL 990
Db 1171 IPASSMPQOQIGPTS-----SLTQVWHSAGR-RTIVSPVPSRERESKVFPSEETD TV 1222

Qy 991 ELQOKANSNLSLQOREANALAMOKWNSLBDGRHLTLNLTSKIELINGELOQSDYTEDA TD 1050
Db 1223 AASTANGPMNISHASSLSIQQAFF-----ELRRAQM-----TEGPNT 1261

Qy 1051 TKPDRD-----IELBSALDTPDEPGQSEPIEILD--TQGJISQNDQ 1092
Db 1262 APPNFSTHTGTPVPPVPPFLSSIAGVPTAAATAPVUTSSPPNDISTSVIOSEVTVPTE 1321

Qy 1093 LIJNGMAVENGHPVQHQKEPKQKKSQSLGEDHVILEBQKILPVTSQFCQPLPVISMAS 1152
Db 1322 GIAGVATSTGVTGSGLPP-----VSESPVLSSWVSSITPAVVSISTS 1368

Qy 1153 -CLPITTSVS 1161
Db 1369 PSLQVPTSTS 1378

APPLICANT: Van Sligterhorst, Isaac
 TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
 FILE REFERENCE: LEX-038-078-USA
 CURRENT APPLICATION NUMBER: US/00/010,720
 CURRENT FILING DATE: 2002-05-21
 PRIOR APPLICATION NUMBER: US 60/206, 015
 PRIOR APPLICATION NUMBER: US 09/854, 856
 PRIOR FILING DATE: 2000-05-14
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 36
 LENGTH: 2185
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)..(2185)
 OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-10-010-720-36

Query Match 3.1%; Score 194; DB 2; Length 2185;
 Best Local Similarity 18.5%; Pred. No. 1.e-05; Mismatches 506; Indels 362; Gaps 49;
 Matches 235; Conservative 167; MisMatches 506; Index 362; Gaps 49;

Qy 48 KKCPCPDQTAINT-----DIDVLPVNFAFLQLVGAQDPHOSIKLNLGEN 92
 Db 315 KRSAPAKSVIGKPEPMAPEMVEKYDVSQDVYAFGMCMLEMTASEPV----- 361
 Qy 93 KHYEVAKKCVVEDALAYVKPLSGKGKVAVSNLGSAL-----SRPMQKLVLVN 139
 Db 362 -----YSECQNAAQIVRVTGSKV-PASFDKVAIPEKEIIGCIRQNDRYSIKDLN 415
 Qy 140 CQLEVERBGRVRAMRAARSLSGLBTETVTEILORHNPOLSANLWAIAVRARGCQFLGRAMOEE 199
 Db 416 HAFFQEBTGVVRVELAEEDEGKEKIAKWLRLBDIKLK-----GKVKDNE 460
 Qy 200 ALKLVVLALEFGSALSRLKVLVLFVQRLPEPQASAKTSIGHVWQLYRASCFCVKVDR 259
 Db 461 AIEF-----SFDLERDVPEDVAOENVESEGVUCBGDHDHTWAKAIKDR-- 501
 Qy 260 DSSLMQKEEPRFSYEALRREHDQAQTHIAMEAGLRISPEQWSLLYGDLAHKSHMOSIID 319
 Db 502 -VSLIKRKREOR- -OLVREBEEKK-----KOBESSLHQVEGSSAOTGIK 544
 Qy 320 KLIOSPEFAKSVVOELTIVLORTGDP-----ANLNRLRPHLELLANIDNPDAVSPTW 371
 Db 545 QLPSASTIGIPIASTTSASVSTQVEPEPPEADQHQQLQQYQPSISLVS-DGTVDQGSS 602
 Qy 372 EQLENAMAVKUWVHGLDFIQNYSKGHET-----POQPNCKXKTSMCRDL 419
 Db 603 VFTESRVSSQQTQSYG-----SQHEQAHSTCTVPGHIPSTVQAOQSOPHGVTYPPSSVAQG 656
 Qy 420 RQQGCGRGTTCTFAMSQEELKYLLENKKINATVTFPLINKVGUNNTVTAGNIVS 479
 Db 657 QSQGQ_PSSSTGTGVSSQPQHQ-----CQQGQQTAPQQ----- 692
 Qy 480 IGSTETGKIVPSTNGISNAENVSQQLSRSSTDSTRALETVKKVSKVKGANGQNAAGPSA 539
 Db 693 -----QTQVQSLSQ-TSISSEAT-----TAQPVQSPQOA 719
 Qy 540 DSVTENKIGKSPPKTPVSNVAAASAGPSN--VGETELNSVQPKSPEFLTRV-----PVYP 591
 Db 720 PQVLP-QVSAGKQLPVSPQVPTQGEPQIPVATQPSVVPVHSAGAHFLPVQGPQPLPTPLP- 777
 Qy 592 HSEN1QYQFDPTQIPEPVQY-POTGYYPPEPTVAGVACRCPVFRVRNSVNPESLP- 648
 Db 778 -----QYPSQIPISTPHSTAQPGFSSPITPAHGIQ---PULITASSATAI PG 827
 Qy 649 -----PASMPYDHYSTFSPRMRNNPSY---QPPP-----PQPYGVPPVPSGMVAPY 694
 Db 828 VSTVVPSQLP----TULQPVYQLPQVHPQQLQPAVQSMGIPANLQQAABVPLSSGDV 882

RESULT 7
 US-09-854-856-4
 ; Sequence 4, Application US/09854856
 ; Patent No. 6541252
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Hilburn, Erin
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
 ; FILE REFERENCE: LEX-0178-USA
 ; CURRENT APPLICATION NUMBER: US/09/854, 856
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: US 60/206, 015
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 2245
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)..(2245)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-09-854-856-4

Query Match 3.1%; Score 194; DB 2; Length 2245;
 Best Local Similarity 18.5%; Pred. No. 1.e-05; Mismatches 506; Indels 362; Gaps 49;
 Matches 235; Conservative 167; MisMatches 506; Index 362; Gaps 49;

QY 48 KACPFDQATAINT-----DIDYLPUVFALLQVGAQVPDFHOSIKLUSNLGEN 92
 Db 375 KRASFAKSVIGTPEFMAPEMVEKYDESDVYAFGMCMLEMMATSEYP----- 421
 QY 93 KHYEVAKKCVEDLAJLKPLSGKGKVASLNQSL-----SRPMORKUTLVN 139
 Db 422 ----YSECONAQIYRRTSGVK-PASFDKVAIPEVKETIEGCTRONKDERYSIKDLN 475
 QY 140 CQVLEEEGRVRAMAARSLGLERTVTBELLQHNPQOLSANLWAUVRARGCQFLGPAMQEE 199
 Db 476 HAFFQETGVRLVLAEDGEKIAIKLWRERDIKLU-----GKYKDNE 520
 Db 521 AIEF-----SFDLERDVDPEDAQAQMENVEGIVCEGDHKTMKAIKDR-- 561
 QY 260 DSSLMLQKEEFSYEALRREHDQVHIMAGLRSPEQMSLJGDLAKSHMOSIID 319
 Db 562 -VSLIKRKREOR-OLVREEOKK-----KOSESSLKOQVEOSSASOTGK 604
 QY 320 KLUQSPESPAKSVOELTIVLQRTGDP-----ANINLRPHELLANIDNPDAVSPTW 371
 Db 605 QLPSASTGIPFASSTASVOSTOPEADPOHQYQOPISLUS-----DGTVPDSQGSS 662
 QY 372 EQLENAMAVKTVVHGLVDFTIONYSRKGHET-----POPOPNSKXKTSMCRDL 419
 Db 663 VFTESRVSSQQTSYG----SQHOAHSTGTVPGHIPSIVQAOQSPHGWYPPSSVAQG 716
 QY 420 RQCGSGPRGNTCTFASSQEELEKRYARNKKNAATVTFPLINKVQNTNTVTAGNIVS 479
 Db 717 QSQGQ-PSSSLSTGVSSQSPQHQPO-----QOOGIQTAPPQ----- 752
 QY 480 IGSTETRGKIVPSTNGSINAENNSVQLISRTDSTALETWKVKGANGQNAAGPSA 539
 Db 753 -----OTVOSLSD-TSTEAT-----TAQPVSPQOA 779
 QY 540 DSVTENKIGSPPTKTPVNSVAATSGASN-----VGETLNSVPOQKSPFLTRV----PVYPP 591
 Db 780 PQVLP-QVSAGKQLPSPQVPTIQGRQPIVATQPSVPSVPSGAHLPLPGQPLPILP- 837
 Qy 592 HSENIOYFQDPRTQIPFPEVPOY--PONGYPPRPPTVAGVACVCPVFRVRSNVPESLP- 648
 Db 838 -----QYPSQIPISTPHVSTAQGFSSLIPITMAGIQO--PULTASSATTAAIPG 887
 Qy 649 ----PASMPYDHYSFSPRRMNSPY----QPPP-----PQPGVPPVPPVPSGMVAPV 694
 Db 888 VSTVUVSOLP-----TILQPVTPSPVHPQLOPAVQSMGJANTQQAETPLSSGDLV 942
 QY 695 YDSRRRIWRPPMMQRDDIIRNSLSLPPMDVMHSYYQTSURERYNSLOGYSYACOPSEPR 754
 Db 943 YQGFPPRPLPQPGPSMIAPESSNVASYCITHSTVLPMPMTVLTATGCFPTVQPTYESN 1002
 QY 755 TTVPL-----PRERCGHL---KTSCEBOIRRKRDQWAOYHTQKAPVYSTLVPATO 802
 Db 1003 LIVPMGGVGGOVQVSQFGSLAQAPTSSQQAVLES-----TOQVSQVAPAENVAVA 1054
 Qy 803 SP---TPPSPL-FSDF-----RADPSESTSGTKFEEDHSHYSPWSGCGIGSCINAI 851
 Db 1055 QPQATOPIITLASSVDSAHSDVAGSMQDGNNPSSRSGRHEGTTKRYKRSRSRHEK 1114
 QY 852 DSEPKDVIAN-----SNAVIMLDGSDGVKRRVHLFETORTTYKEEDPLIPFSDGPIISKW 906
 Db 1115 TRPKLKRITLNVANKGDRTVECCLETHRKMVTPKFDPDGDPAEELATIMVNNDLF--- 1170
 QY 907 AISRSS-----RTSYHTDPVQA-----TASQ-----GATKP 934
 Db 1171 AIEFESTFDQVRLIEKADEMMSEDVSVEPEGDQGLESLOGDGYFGSGQXLEGEPFKP 1230
 QY 935 ISVSDVYPPVNAVDSRNSYSGEATSSAHYVDRFVTUDSGHRKSS--TGDU-SL 990
 Db 1231 IPASSMPOOIGPTS-----SLTOVHHSAGR-RFIYSPVVERSKVPESETDTV 1282
 QY 991 ELQAKNSNLQOREANALAMQKUNSLDRERHLTINLISKEIJRNGLQSDYTEDAID 1050
 Db 1283 AASTROSPGMNLSHASSLSLQOAS-----BERRAM-----TEGPNT 1321
 QY 1051 TKPDRD-----IEBLSLADTDPEPDQSBPIEILD-TOLGISSNDQ 1092
 Db 1322 APPNFSHGPPTRPVVPPFLSSIAGVPTAAATPVATSPSOPNDISTSVQSEVVPTEE 1381
 QY 1093 LLNGMADVNGSHIPVOQHOKERPKQKQSLGEDHVLBEQKUILPVPSFCSPOLPVSIAS 1152
 Db 1382 GIAGVATSTGVVTSGGLPIP-----VSESPLVSSVSSITIPAVSISTS 1428
 Qy 1153 -CLPITTSVS 1161
 Db 1429 PSLQVPTSTS 1438

RESULT 8
 US 10-010-720-4
 ; Sequence 4, Application US/10010720
 ; Patent No. 6858419
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Hilbun, Erin
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Hansen, Gwenn
 ; APPLICANT: Beltrando Rio, Hector
 ; APPLICANT: Van Sligtenhorst, Isaac
 ; TITLE OF INVENTION: Encoding the Same, And Uses Thereof
 ; TITLE OF INVENTION: Encoding the Same, And Uses Thereof
 ; FILE REFERENCE: LEX-0382-USA
 ; CURRENT APPLICATION NUMBER: US/10/010-720
 ; CURRENT FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: US 60/206,015
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIORITY NUMBER: US 09/854,856
 ; PRIORITY FILING DATE: 2000-05-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 2245
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)..(245)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-10-010-720-4
 Query Match 3.1%; Score 194; DB 2; length 2245;
 Best Local Similarity 18.5%; Pred. No. 1.1e-05; Gaps 49;
 Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;
 Db 755 TTVPL-----PRERCGHL---KTSCEBOIRRKRDQWAOYHTQKAPVYSTLVPATO 802
 Qy 48 KACPFDQATAINT-----DIDYLPUVFALLQVGAQVPDFHOSIKLUSNLGEN 92
 Db 375 KRASFAKSVIGTPEFMAPEMVEKYDESDVYAFGMCMLEMMATSEYP----- 421
 Qy 93 KHYEVAKKCVEDLAJLKPLSGKGKVASLNQSL-----SRPMORKUTLVN 139
 Db 422 ----YSECONAQIYRRTSGVK-PASFDKVAIPEVKETIEGCTRONKDERYSIKDLN 475
 Qy 140 CQVLEEEGRVRAMAARSLGLERTVTBELLQHNPQOLSANLWAUVRARGCQFLGPAMQEE 199
 Db 476 HAFFQETGVRLVLAEDGEKIAIKLWRERDIKLU-----GKYKDNE 520
 Qy 200 ALKLVLIALEDGSALSRKVVLVFVVRLEPRPQASKTSIGIVVQLYRASCFCVKTRDE 259
 Db 521 AIEF-----SFDLERDVDPEDAQAQMENVEGIVCEGDHKTMKAIKDR-- 561
 Qy 260 DSSLMLQKEEFSYEALRREHDQVHIMAGLRSPEQMSLJGDLAKSHMOSIID 319
 Db 562 -VSLIKRKREOR-OLVREEOKK-----KOSESSLKOQVEOSSASOTGK 604

GENERAL INFORMATION:
 APPLICANT: Walke, D. Wade
 APPLICANT: Hilburn, Erin
 APPLICANT: Turner, C. Alexander Jr.
 INVENTOR: Human Kinases and Polynucleotides
 TITLE OF INVENTION: Encoding the Same
 FILE REFERENCE: LEX-0178-USA
 CURRENT APPLICATION NUMBER: US/09/854,856
 CURRENT FILING DATE: 2001-05-14
 PRIOR APPLICATION NUMBER: US 60/206,015
 PRIOR FILING DATE: 2000-05-19
 NUMBER OF SEQ ID NOs: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 34
 LENGTH: 2322
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)..(2322)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-854-856-34

Query Match 3.1%; Score 194; DB 2; Length 2322;
 Best Local Similarity 18.5%; Pred. No. 1..1e-05; Mismatches 506; Indels 362; Gaps 49;
 Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

Query	Subject	Start	End	Length	Similarity	Mismatches	Indels	Gaps
QY	48 KACPDPQTANT-----DIAWLPVNFALLQWAGQVDPHQSSIKLSNLGEN 92							
Db	315 KRASFAKSVGTGTTPEFMAPENYEKYDESIVYAFGCMCLMENATSEVP----- 361							
QY	93 KHYEVAKKCEDLAIYLKPLGGKVVASLNQSALE-----SRDMQRKVLTWN 139							
Db	362 -----YSECONAQIYRRVTSVGKV-PASEPKVATEPKKEIEGCIRQNDKRDYSIKDLN 415							
QY	803 SP---TPPSPL-FSVDF-----RADFSESVSGTKFEEDEHLSAYSPWCGTIGSCINAI 851							
Db	1055 QPQTAQPTTLASSVSDAHSVAGSMIDGNENVPPSSGRHEGRTTKRHYKSVRSRRHEK 1114							
QY	852 DSEEKDVIAN-----SNAVIMLDLSSGDVVKRVRHETEQRTKEDDPIIFSDGKIIKNG 906							
Db	1115 TSRPKRILANVSNKDRVVCEQLETHNRKAVTFKEDLDGDNPEEATIMNNDFL---- 1170							
QY	907 AISSS-----RTGYHTDPQA-----TASQ----GSATKP 934							
Db	1171 AIEERSFVQPRETEKADMLESDVSVERPEGDGCGLESQKGDDYGFSSQKLGEGRKQP 1230							
QY	935 ISVSDIYPVNAUDSRWSSYGNNEATSSAHVERDFITDLSGHRKHSS---TGDL-SL 990							
Db	1231 IPASSMPQQIGIFPS-----SLTOVHSAGR-RFIVSPVPESSRLRESKVUPFSEITDV 1282							
QY	991 ELOQAKSNLLOPERBANALAMQKVNLSDEGRHITLNLISKEIIRLNGLQLQSDYTEDAID 1050							
Db	1283 AASTAQPQMLSHASSLSQLQAFS-----ELRAOM----TEGPNT 1321							
QY	1051 TKPBD-----IEBELSALDTDBPDQSBPIEILD--IOLGISQNDQ 1092							
Db	1322 APPFHSTGPTFPVPPFELSIAGVPTTAATAPVPAESPPNNDISTSVIQSEVTWPTER 1381							
QY	1093 LLNNGAVENGHPVQOQHQKEPKQKKQSGLGDHVILIEQKNTILPYTSCFSQQLPYSISNAS 1152							
Db	1382 GIAGVATSTGVWVGGGLPIPP-----VSESPVLSSVSSITIPAVVISITS 1428							
QY	1153 -CLPITTSVS 1161.							
Db	1429 PSLOQVPTSTS 1438							
QY	RESULT 9							
QY	US-09-854-856-34							
QY	Sequencher 3.4 Application US/09854856							

540 DSVENTKLGSPPKTRVSNVAAATAGPSN--VGTELNSVQPKSSPFLTRV----PVYPP 591
 720 PQVLP--QVSAGKQLPVSQVPPFTIOPPFEPVQY--POTGYPPPPVPGAVCPVERFVSNVPESSLP- 648
 592 HSENQYFOPRTOIPPFEPVQY--POTGYPPPPVPGAVCPVERFVSNVPESSLP- 648
 778 -----QVYVQSLSQ-TS-SSEAT-----TAQPVSQPQ 779

QY 649 ----PASMPYADHYSTFSRDRMNSPPY----OPPP----PQYGPVPPVPSGMAYP 694
; : : ; : : ; : : ; : : ; : : ; : : ; : : ; : : ; : : ; : : ; : : ; :
; LOCATION: (1)..(232)
; OTHER INFORMATION: Xaa = Any Amino Acid .
; US-10-010-720-34
; Query Match 3.1%; Score 194; DB 2; Length 2322;
; Best Local Similarity 18.5%; Pred. No. 1.1e-05;
; Matches 235; Conservative 167; Mismatches 506; Indels 362; Gap 49;
; Db 828 VSTVVPSQLP----TLLQPTQLPSQVHQLQPAVQSMGIPANLQAAEVPLSSGDL 882
; QY 695 YDSRRTWRRPMYORDDIRSNSLPPMDVMHSVYQTSRLERYNSLDGYSVACQPSEPR 754
; 883 YQGFPPLRPPQPGDSNIAPSSNVAVCISHTVLXPPMPTBEVALTPGYFFTVQVYESN 942
; 755 TVPL----PREPCGH----KTCSEQRIRRKPDQWAOYHTQKAPLYSTLPVATQ 802
; Db 943 LLVPMGGVGGOVQSQPGSLAQAPTTSQOAVLES----TOGSVQAPAEPVAVA 994
; QY 803 SP----TPPSPL-FSVD----RADFSEWSVSGTKFEEBDHLSHSPWMSCTIGCINAL 851
; 995 QPQATOPTTLASSVDSAHSDVASYGMSDGNENVPSSGRHGRCTKHYRSRSRHEK 1054
; QY 852 DSEPKOVIAN----SNAVLMDLDSDGVKKRVLHFETQRTRKEEDPIIPIFSDGPIISKWG 906
; 1055 TSRPKLILNVNGKDRVVECOLETHRKRTFKFDLGDPEEATIMVNDFL--- 1110
; 907 AISRSS----RVCYHTTDPVDA----TASO---GSATKP 934
; Db 1111 AERESFVDOVREIEKADEMLEDVSVEPEGDQGLESLOGKDYGFSGSQLEGEFKQ 1170
; QY 935 ISVSDVVPVYNAVDSRWSSYGENAISSAHYERDFTVTDLSGHKRHS--TGDL-SL 990
; 1171 IFPASMSMQQICGPTS----SLTQVHSAGR-RFIVSPVRESRKEVSEITDV 1222
; QY 991 ELQQAKNSNLQOREANALAMQOKWNSLDEGRHLTUNLISKELRNGELOSSYBATO 1050
; 1223 AASTAQSPGMNLSHSASLSSLQOAFS----ELRAQM---TEGPNT 1261
; Db 1051 TRPDRD----IELELSALDDDEPDCOSEPTEELD--IOLGIISONDQ 1092
; QY 1262 APPNFSTHGPTPPVVFPLSSTAGVPTTAATAPVATSSPNDISTSVIOSEVTVPTE 1321
; QY 1093 LINGMAVENGHIVVQHQIKERPKQKKSILGEDIVILSERQKTIPLVNSCSQPLPVSI 1152
; 1322 GIAGVATSTGVVTTSGGLPIPP----VSSEPVLSVSSSITIPAVSISTS 1368
; QY 1153 -CLPITSVS 1161
; Db 1369 PSLQVPTSTS 1378

RESULT 10
US-10-010-720-34
; Sequence 34; Application US/10010720
; Patent No. 6558419
; GENERAL INFORMATION:
; APPLICANT: Walk, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hansen, Gwenn
; APPLICANT: Beltranelli, Hector
; APPLICANT: Van Sligtenhorst, Isaac
; TITLE OF INVENTION: Encoding the Same, And Uses Thereof
; FILE REFERENCE: LEX-0362-USA
; CURRENT APPLICATION NUMBER: US/10/010,720
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/654,856
; PRIOR FILING DATE: 2000-05-14
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 2322
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: VARIANT
; LOCATION: (1)..(232)
; OTHER INFORMATION: Xaa = Any Amino Acid .
; US-10-010-720-34
; Query Match 3.1%; Score 194; DB 2; Length 2322;
; Best Local Similarity 18.5%; Pred. No. 1.1e-05;
; Matches 235; Conservative 167; Mismatches 506; Indels 362; Gap 49;
; Db 4 KACPDTAINT----DIOLVNPNALQLVAGQVDPHQSIKULNLGEN 92
; Db 315 KRASFANKVIGTPERMAPMEEEKYTESDVSYAFFGKNCMLMATSEPV----- 361
; QY 93 KHYEVAKKCVEDALYLKKPLSGGKGVASLNASL-----SRPMQRKVLTVIN 139
; Db 362 ----YSECQMAQIYRRVTVSGVK-PASEKVALAEVKEIEGCRQNQKOBRYSTKDLN 415
; QY 140 COLVERBERGVYRAMAARSLSGERTVBLLOHONPOOLSANLWAAYARGQFLGANQEE 199
; Db 416 HAFFQETGVVELAABEDGKIAKLUKLIEDIKLK-----GKYKDN 460
; QY 200 ALKLVVLALEGSALSRSKVNLFVWYORLERFPOASKTSIGHVWOLYRASCFCYTKRDE 259
; Db 461 AIEF-----SFDIERDVFEDVAGEMVEMSCYVCSDHKTMKAIAKDR-- 501
; Db 260 DSSLMQIKEERSYEALRREHAQIYHIAAMEAGLRISPEOMWSSLLYGDLAHKSHMOSID 319
; Db 502 -VSLIKRKREGR---QLVRESEQEK-----KOBESSLKQVOFOSSASQTGIK 544
; QY 320 KLOQSPESPFAKSVQELTIVLQRTGDP-----ANILRRLPHLELANIIPNPDAVSPTW 371
; Db 545 OLPSASTGIPPASTTSASVSTQVERPEPADOHQQLQYQQPSISLS--DGTVDQGQSS 602
; QY 372 EOLENAMAVKUVVHGLUDFTONYRSKGHER-----POPOPNSKYKTMCRL 419
; Db 603 VFTESRVSSQOTVSYG----SOHQRAHSTGTVPCHIPISTVQAQSOPHQYPVPPSSVAQ 656
; Qy 420 ROQGCPRGIGNTFAHSQEEKYLURNNKINATVTFPLNKVGVNNTVTTAGNIVS 479
; Db 657 QSOGO-PSSSLITGVSSQOPTOHPO-----OOQGIOQATAPQO----- 692
; Qy 480 1GSTETGKIVPSTNGTISNAENSVSOLISRSTDSTIARLETVKKVKGANGQNAAGPSA 539
; Db 693 -----QTVQYLSQ-TSISSEAT-----TAQPVSQPQA 719
; Qy 540 DSVTENKIGSPPKTPVSNVAAATSAGSN--VGTELNSVPOQKSPFLTRV-----PVYPP 591
; Db 720 PQVLP-----QVSAKGQLPVSQVQVPTIQGQRPQVATOPSVWVPSGAHLPLVQGPLPTPLP- 777
; Qy 592 HSENIQYQDRTQIPEPVQY--POTGYYRPPPTVAGVAPCVPRFRSNVNPESLP- 648
; Db 778 -----QPVSQPISTPHVSTAQGFLSLPITMAGITQ--PLTLLASSATTAIIG 827
; Qy 649 ----PASMPYADHYSTFSRDRMNSPPY----OPPP----PQYGPVPPVPSGMAYP 694
; Db 828 VSTVVPSQLP----TLLQPTQLPSQVHQLQPAVQSMGIPANLQAAEVPLSSGDL 882
; Qy 695 YDSRRTWRRPMYORDDIRSNSLPPMDVMHSVYQTSRLERYNSLDGYSVACQPSEPR 754
; Db 883 YQGFPPLRPPQPGDSNIAPSSNVAVCISHTVLXPPMPTBEVALTPGYFFTVQVYESN 942
; Qy 755 TVPL----PREPCGH----KTCSEQRIRRKPDQWAOYHTQKAPLYSTLPVATQ 802
; Db 943 LLVPMGGVGGOVQSQPGSLAQAPTTSQOAVLES----TOGSVQAPAEPVAVA 994
; Qy 803 SP----TPPSPL-FSVD----RADFSEWSVSGTKFEEBDHLSHSPWMSCTIGCINAL 851
; Db 995 QPQATOPTTLASSVDSAHSDVASYGMSDGNENVPSSGRHGRCTKHYRSRSRHEK 1054
; Qy 852 DSBRPKDVTAN----SNAVLMDLDSDGIVKRRVLHFETQRTRKEEDPIIPIFSDGPIISKWG 906
; Db 1055 TSRPKLILNVNGKDRVVECOLETHRKRTFKFDLGDPEEATIMVNDFL--- 1110

QY 907 AIRSRS-----RTGYHTDPVQA-----TASO---GSATKP 934
Db 1111 AIERSFVDQREIEKADEMLEDVSVEPREGQGLESLOCKDDYGFSGSKLEGFKQ 1170
QY 935 ISVSDYVPPYNAVDSRWSSYGNNEATSSAHYERDRDITVLDGHRRHSS---TGDLI-SL 990
Db 1171 IPASSMPQIGIPTS-----SLTQVHHSAGR-RFTIVSPVPESRLESKVFPSEITDV 1222
QY 991 ELQOKNSNLILQREANALAMQKWNLSLDEGRHLTLNLSKEIELRNGELOSDDYEDATO 1050
Db 1223 AASTAQSPGMNLHSASSLSQLQAFS-----ELRAQM---TEGPNT 1261
QY 1051 TKPDRD-----IEELSALDTDEPDGQSPRIEILD---IOLGISSONDO 1092
Db 1262 APPNFSHSTGTPFPVVFPLSSIAGVPTTAATAPVPATSSPPNDISTSVIOSEVUTPTEE 1321
QY 1093 LLNGMADVNGHPVQHQKEPPKKQKQSLGEDDHVILEBQTKILPVTSCEFSOPLPVISNAS 1152
Db 1322 GIAGVATSTGVVTSGGLPIPP-----VSESPVLSSVWSITIPAVWSISTS 1368
QY 1153 -CLPITTSV 1161
Db 1369 PSLOVPTSTS 1378

RESULT 11
US-09-854-856-2
; Sequence 2, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walkie, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Dnoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: DEX-017-8-USA
; CURRENT APPLICATION NUMBER: US/09/854, 856
; PRIOR APPLICATION NUMBER: US 60/206, 015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2382
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)..(2382)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-854-856-2

Query Match 3.1%; Score 194; DB 2; Length 2382;
Best Local Similarity 18.5%; Pred. No. 1.2e-05; Mismatches 506; Index 362; Gaps 49;
Matches 235; Conservative 167; Mismatches 506; Index 362; Gaps 49;

QY 48 KACPDPQTANT-----DIDVLPVNFAFLLOLVGAQVDPHDOSIKLUSNLGEN 92
Db 375 KRASPAKSVIGTPEPMAPEMYEKEDSYVYAFGMQMLEMATSYV-----421
QY 93 KHYEVAKCYEDALYLKLPLSGKGKGVASINQSL-----SRDMDRKULVTLN 139
Db 422 ---YSECQMAQIYRRTVSGVK-PASFDKVAlPEVKETIEGCTRQNKRDKYKDLN 475
QY 140 CQLVEREGRTRAMRAARSLGERTTYBLIQHQNPOLSAMWAAVTRARGSOFLGAMQEE 199
Db 476 HAFFOBETGVVRLVELABEDDGSEKIAKUWLRIEDIKLK-----GKYKDNE 520
QY 200 ALKULVLALEDGSGALSRKVLVFLVQRLERPFQASKTSIGHVWOLYRASCFKVTKRDE 259
Db 521 AIEF-----SFIDERDVPEVDVAEBMEVGGVCGDKHMKWAKAKDR-- 561

QY 260 DSSLMOIKEERSYEALRREHDAQIVHIANEAGLRISPQEONSSLXGDLAIIKSHMOSID 319
Db 562 -VSLIKRKREOR-QLVREEQEKK-----KOBESSIKQVOEOSSA-SOTGK 604
QY 320 KLOSPASRFKASVQELTIVLQRGTGDP-----ANLNRRLPHLELANTIPNPNDVSPTW 371
Db 605 QLPSASTGIGTAST-SASVSTQVEPEPEADQHQQLYQOOPSISIVS-BCTVDSQGSS 662
QY 372 EOLENAMAVKTVVHGLDFQNYSRKGHET-----PQPQPNSKYKTSMCRDL 419
Db 663 VFTESERVSQDQTVSG-----SQBQAHSTGTVPHIRSTVQADSSQPHGVYPSSVAQG 716
QY 420 RQOGCPCRGNTCTFAISQEELEYKVRNKKINATVTFPLUNKVGUNNTVTTAGNVI S 479
Db 717 QSQGQ-PSSSLTGNSSSQIOPHQ-----QQGIIQQTAPPQ---- 752
QY 480 IGSTETGKIVPUSTNGISINAENSQSLISHSTDSTLRALETYKKGKVGANGONAGPSA 539
Db 753 -----QTVQYLSQ-TSSEAT-----TAQPVSQ 779
QY 540 DSVTEENKIGSPPKTPSNNVAATSAGPSN-----VGETLNSPVOKSSPFLTRV-----PVYPP 591
Db 780 PQVLP-QVSAKQLPVQSPQPTICERPOVATQSPWVPHGAHFLPQSCQPLP 837
QY 592 HSENIQYFQDPRTOFPEVPOY---POTGYVPPPTVPGAVPCVPRFRVSNVPESPL- 648
Db 838 -----QPVSPQIPISTPVUSTAQTFQSLPITMAIGTQ---PLTASSATTAI PG 887
QY 649 -----PASMPYADHYSTFSRDRMMSSPY-----QPP-----POPVGPVPRPVSGMVPA 694
Db 888 VSTVWPSQLP-----TLLQPTMQLPSQVHFQOLLOPAVQSGMIPANIGQAEVPLSSGDVL 942
QY 695 YDSRRIWPRPMQYRDIRIIRNSLPPMDVMISSVYOTSLSRERYNSLDGYSYVACQPSPE 754
Db 943 YQGFPRPRLPQYGDNSIAPPSNNAVSVCIISTVULPPMPTEVATPGYPRPVQPVESN 1002
QY 755 TTVP-----PREPCGH-----KTCBEOIRRKPDQMAQHTOKAPLAUSLSTPVATQ 802
Db 1003 LLVPGPGVGEQVQVQSPQGGLAQAPITTSQAVL-----TQGVQVAPBPAVA 1054
QY 803 SP---TPPSPL-FSVP-----RADFSSRSVSGTKFEDHLSHYSPWSCOTGSCINAI 851
Db 1055 OPQATOPTTLASSVSDAHSVAGMSDGMNIVPSSGRHGCRTRKHYRSVRSRHEK 1114
QY 852 DSEPKDVIAN-----SNAVUMLDGSGDVKERVHLFETQRTRKEEPIPLPSDGPIISKWG 906
Db 1115 TSRPKURILNVSNKDRVBCOLETHNRKAVTFKFEDLGDNPPEEATIMWINDFL--- 1170
QY 907 AIRSRS-----RTGYHTDPVQA-----TASO---GSATKP 934
Db 1171 AIERSFVDQREIEKADEMLEDVSVEPREGQGLESLOCKDDYGFSGSKLEGFKQ 1230
QY 935 ISVSDYVPPYNAVDSRWSSYGNNEATSSAHYERDRDITVLDGHRRHSS---TGDLI-SL 990
Db 1231 IPASSMPQIGIPTS-----SLTQVHHSAGR-RFTIVSPVPESRLESKVFPSEITDV 1282
QY 991 ELQOKNSNLILQREANALAMQKWNLSLDEGRHLTLNLSKEIELRNGELOSDDYEDATO 1050
Db 1283 AASTAQSPGMNLHSASSLSQLQAFS-----ELRAQM---TEGPNT 1321
QY 1051 TKPDRD-----IEELSALDTDEPDGQSPRIEILD---IOLGISSONDO 1092
Db 1322 APPNFSHSTGTPFPVVFPLSSIAGVPTTAATAPVATSSPPNDISTSVIOSEVUTPTEE 1381
QY 1093 LLNGMADVNGHPVQHQKEPPKKQKQSLGEDDHVILEBQTKILPVTSCEFSOPLPVISNAS 1152
Db 1382 GIAGVATSTGVVTSGGLPIPP-----VSESPVLSSVWSITIPAVWSISTS 1428
QY 1153 -CLPITTSV 1161
Db 1429 PSLOVPTSTS 1438

RESULT 12
US-10-010-720-2
; Sequence 2, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hennen, Gwenn
; APPLICANT: Beltrandelio, Hector
; APPLICANT: Van Sligghorst, Isaac
TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
TITLE OF INVENTION: Encoding the Same, And Uses Thereof
FILE REFERENCE: LEX-0388-2000-USA
CURRENT APPLICATION NUMBER: US/10/010,720
CURRENT FILING DATE: 2002-05-21
PRIORITY APPLICATION NUMBER: US 60/206,015
PRIORITY FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/854,856
PRIOR FILING DATE: 2000-05-14
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2382
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(2382)
; OTHER INFORMATION: xaa = Any Amino Acid
; US-10-010-720-2

Query Match 3.1%; Score 194; DB 2; Length 2382;
Best Local Similarity 18.5%; Pred. No. 1.2e-05; Mismatches 506; Indels 362; Gaps 49;
Matches 235; Conservative 167; Mismatched 506; Indels 362; Gaps 49;

QY 48 KACPFDTAINT-----DIDVLPNFAALLQVGAQVDPHOSIKLNSLGEN 92
Db 375 KRAFSAFKSVIGTPEPMAPEMYEEVKYBDSVDTYAFGNCMMLWATSEYP----- 421
QY 93 KHYEVAKKCVEDALAYKPLGGKGWASLNSSAL-----SRPMQRKVLTVN 139
Db 422 ---YSECQNAQIYRRTVISGVK-PASFDKVAIPKEIEGCIRQNKRDKYISKDLN 475
QY 140 CQOLVEEGRVRVRAARSLGLRTVTELLILQHNPOLSANLWAVERARGCFLGRAMOEE 199
Db 476 HAFFOETGTVRVELABEDDGEGKIAKUWLREBDIKLK-----GKVDNE 520
QY 200 ALKUVLVALEDGSALSRKVLFVFVQRLPREPQASKTSIGHVQLYRASCFFKVKRDE 259
Db 521 AIEF-----SFDLRDVPDVAQENVEGVCBEGDHTKMKAIKDR-- 561
QY 260 DSSLWQIKEETRSYEALRREHDQAQIVHIALMAGLRTSPEONSLLYGDLAIIKSHMOSIID 319
Db 562 -VSLIKRKREQR-OLVREEQKK-----KOSESSLIQKQVEQSSASOTGIK 604
QY 320 KIQPSFAKSYQELTIVLQRTGDP-----ANLNRTRPHLELANTIDNPDAVSPTW 371
Db 605 QIPSSASGIPTTSTSASVSTOVEPEPPEADOOHQOLQYQQOSSISVIS-----DGTVDSQGSS 662
QY 372 EOLENAMAVKTVVHGLDFIONYSRKGHET-----POPOPNSKWTSMCRDL 419
Db 663 VFTESRVSSQQTQSYG-----SOHOBAHSTGTVPGHIPSTVQAQSOPHGVYPPSSVAQ 716
QY 420 RQQGCCPRGTTNTFQHSQBELLYKJRNKKNATVRTFPFLINKRKGVNNTVTAGNIVS 479
Db 717 OSOGQ-PSSSLTGVSQSQPIQHQ-----QQQGQIQTAPPQ----- 752
QY 480 ICSTETTGKIVPSTNGISNAENVSQNLISRSSTDRALETVKVKVGANGONAGPSA 539
Db 753 -----QTVQSLSQ-TSTSSEAT-----TAQPVSQPA 779

RESULT 13
US-09-854-856-48
; Sequence 4, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
LENGTH: 1939

QY 540 DSVTENKIGSPPKTRPVSNVATSGPSN--VGETEANSVOKSSPPLTRV-----PVYPP 591
Db 780 PQLP-QVSAGKOLPVSQVSPYTOCERPQVATOPSUVPHSGAHFLPVQGPQPLTPLP- 837
QY 592 HSENIQYFQDPTQIPFEVHQY---POTGYVPPPTVPGASVAPCPVFRVNNVPESSLP- 648
Db 838 -----QYVPSQPISTPHVSTAQTGSSLPTIMAQITQ--PLLTASSATAAIG 887
QY 649 -----PASMPYADHYSTFSRDRMNSSPY---OPPP---PQPYGPPVPSGMYAPV 694
Db 888 VSTVVPSQLP-----TLLQPVTLQPSQVHQLQPAVQSMGIPANLGQAEVPLSGDVL 942
QY 695 YDSRRIWRPPMVQRDIDINSLPPMDVMISSVWOTSLRERYNSLDGYSVACOPPSEPR 754
Db 943 YOGFPPRLPQPGDSNIASSNVASVCTHSTVLPXPPMPEVLAUTGYPEFPVUVQYVESP 1002
QY 755 TVVPL-----PREPCGHL---KTSCBQIRRKPDQWQYHQKAPLVSSTLPUVATQ 802
Db 1003 LLVPMGGVGGQVQVQSPGGLAQAPPTTSQAVLES-----TQGVQVAPAPVAVA 1054
QY 803 SP---TPPSPL-FSVDFR-----RADFSESVSGTKFEDHLSHYSPWSGCTISCIAT 851
Db 1055 QPQATOOPTTASSVSDSAHSDVAGSMGNDGNEVPPSSGRHGRCRTKHKRSVRSRHEK 1114
QY 907 AISRSS-----RTGKHTDPVQA-----TASQ---GSATKP 934
Db 1171 AIESSFDVQRELIEKADEMLESVSEPEGDQLESLOGKDDYGFSGSQKLEGFKQ 1230
QY 935 ISVSDVPPVYNAVDSEWSYNEATSSAHVVERDEFITDLSGRHKS---TGDLL-SL 990
Db 1231 IPASSMRQOQIGPTS-----SLTQWVHSAGR-RPIVSUPESLRESKVFPSEITDVT 1282
QY 991 ELQOKANSLLQOREANALAMOKQNSLDSGRHHTLNLSKIEBERNLGEQSDYEDATA 1050
Db 1283 AASTAOQGMNLHSASSLSLQAFS-----ELRRAQM---TEGPNT 1321
QY 1051 TKPDRD-----IELELSAUBTDPEQDQSPRIEELD---QLGISSONDO 1092
Db 1322 APPNFSEHTGPTTPVWPFLSSIAGVPTTAAATPVATSSPPNDISTSVIOSEVTPTEE 1381
QY 1093 LINGMAVENGHPVQOHQKEPPQKOKSOSLGEDHVILBQKILPVTCPSQPLPVSI 1152
Db 1382 GIAGVATSTGVTSGLPPIP-----VSESPVSSVSSITIPAVWSISTS 1428
QY 1153 -CLPIRTS VS 1161
Db 1429 PSLQVPTSTS 1438

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(1939)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-10-854-856-48

Query Match 3.1%; Score 193.5; DB 2; Length 1939;
Best Local Similarity 19.2%; Pred. No. 9e-06; Mismatches 527; Indels 379; Gaps 57;
Matches 256; Conservative 168; MisMatches 527; Index 379; Gaps 57;

Qy 114 GGKGVASLNGSALSRSRPMRKVLTVNLQVLEEGVR-AMRAARSIGERTVTELQHON 172
Db 660 QOPSSSLTGTGVSQIOPHQOOQGIIQTAAPQQTQYQSLSQTSSEATTAQPSQPA 719

Qy 173 PQOQLPQVSAKGKSTQGVQAVAPAEPAVAVAOPOCATOPTTLASSVDSAHSD--VASGMSDG 776
Db 720 PQOVLPOVSAKGKSTQGVQAVAPAEPAVAVAOPOCATOPTTLASSVDSAHSD--VASGMSDG 776

Qy 228 EPRPPOASKUSIGHVWQLYKRSASCFKVTKRDEDSLMLQK---EPRSYEARREHD 281
Db 777 NENVSSSGGRHEGRHTTKRHYRS-VRSRSHKTRSPKRKLRLNVSNGDRVTECQLETHN 835

Qy 282 AQIVHTAMEAGLIRISBQWSSLY-GDLAKHSHMOSIDKUQSPESFAKSQVQELTVLQR 340
Db 836 RKNNTKFDD-GDNFBEIATIMNNDFILAERESFVDQVREIEKADEMLEDVSVEP 894

Qy 341 TCDPAMLNRLRFPHLELLANTD-----PNPDAVSPWQELENAMAVKT 384
Db 895 EGDQG-----LESLQGDYGFSGSQKULEGEFKQPIAPASM--QQGTPSSLTQV 944

Qy 385 VHGLUDFIQNYSSRGKGETPQOPN-----SKYKTMCRDLRQOGCPRGTCNTFAHS 436
Db 945 VH-----SAGRRFTVSPVBFRESRLESKVFVFPSEIUDTVAATASPQ----MNLSH 991

Qy 437 QEELEYKR-----LRNKKI-----NAVTRTP-----LLNKVGVNNTVTTA-- 473
Db 992 ASSLSIQQAFSEERRAQMTTEGPPNTAAPPNSHGTPTPVVPFFLSSIAVGPTTAATAPV 1051

Qy 474 -----GNVISVIGSTETGKVIPVSTNGISWAENS-----VSQLIS 508
Db 1052 ATSSPPNDISTSVISEVT--VPTEGIAGWATSTGVVTSGGLPIPPVSESPVLSVVS 1108

Qy 509 RSTDPSRALTVKVKKGKVGAN-----GQMAAGPSAD-SVTEENKIG---SPPKTPVSN 557
Db 1109 SITIPAVWSTSTPSLQVPTSTSEIVVSSTALYPTVTSAMSASAGGSTATPGKPPAV 1168

Qy 558 VATSATGSPSNVGYTELNSV-----POKSFPLTRPVVPPHENIQYF 599
Db 1169 VSQQAAGSTTGTATLTSVSTTSFFSTASQSIQLSSTSSTPAAVTWVSAHSUD-KTS 1227

Qy 600 QDPRTQIPFEVYQPYOTGGYPPP-----TVEAGVARPCV-PRFVRSNNVBPSSLPPASMP 653
Db 1228 HSTTGIAFLSL-SAPSSSSPGAGVSSYIISQGGILPLVIFSVIASTPILQAGPTSTP 1286

Qy 654 YADHVTSTESPDRMNSSPYQPPPOSYGPVPPVPSM-----YARVYDS 697
Db 1287 L-----LPQVPSIPLVQFVANPVAQQTLIHSQFQPALPNOPHTHCPEVDS 1334

Qy 698 RRWRWPYQDDI-----IRS -NSLPPMDVMHSS-YQTSLRERYNSLDGYVA-- 746
Db 1335 DT-QPKAPGIDDIKLEEKRSLSSEHSSGAQHASVLSLTVESTVTPGIPTAVA 1392

Qy 747 -----COPPSB-PRTMVPLPREPC--GHUKTSCBEOIRR-KPDDAQHQTOKA 790
Db 1393 PSKULTSTSTCILPPTNLPGLCTVALFVTPTQVSTTQVKPGT---APSKP 1448
Qy 791 PLVSS-TLPVATVOSPPPSPLSVDFADESESVSTKFEEDHLHSHYSPNSCGTGSIN 849
Db 1449 PLTKAPVLPVGTELP-----AGTIPS-E 1470
Qy 850 AIDSEPKDVVIANSNAVLMDDDS-----GDVKKRVLHFETQRRTK--- 888

RESULT 14
US-10-010-720-48
; Sequence 48, Application US/10010720
; Patent No. 6058419

GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilburn, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Hansen, Gwenn
APPLICANT: Beltran del Rio, Hector
APPLICANT: Van Sligtenhorst, Isaac

TITLE OF INVENTION: Human Kinases and Polynucleotides
TITLE OF INVENTION: Encoding the Same, And Uses Thereof

FILE REFERENCE: LEX-0382-USA
CURRENT APPLICATION NUMBER: US/10/010,720
CURRENT FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: US 60/206,015
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/854,856
PRIOR FILING DATE: 2000-05-14
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 1939
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(1939)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-48

Query Match 3.1%; Score 193.5; DB 2; Length 1939;
Best Local Similarity 19.2%; Pred. No. 9e-06; Mismatches 527; Indels 379; Gaps 57;
Matches 256; Conservative 168; MisMatches 527; Index 379; Gaps 57;

Qy 114 GGKGVASLNGSALSRSRPMRKVLTVNLQVLEEGVR-AMRAARSIGERTVTELQHON 172
Db 660 QOPSSSLTGTGVSQIOPHQOOQGIIQTAAPQQTQYQSLSQTSSEATTAQPSQPA 719

* QY 173 POQLSANLWAARVARGCQFQGPA-...-MQEALKVVLUALBEDGSSLRSRKVLVFFVORL 227
 * QY 720 PQVLPQVSAGKQSTQGQVAPAVPAVAVQPAOPTTASSVSAHSD--VASGMSDG 776
 * QY 228 EPRFOASKTSIGHVWOLYRASCVKTRKEDDSSIMQLK----EEFRSYEARREHD 281
 * QY 777 NENVESSSGRHEGRTRKHKRS--VRSRSRHEKTSRPKURILINVSNKGDRVCEOLETHN 835
 * QY 282 AQVHIAEAGLRISPEQWSSLY-GDLAKSHMOSIDKLQSPSEFAKSVOELTIVLQR 340
 * QY 836 RKMVTFKFDLD-GDNPEETATMVNNDFILAIERESFVDQVRETEKADEMSEDSVVERP 894
 * QY 341 TGDPAVLNRPHLELANDID-----PRPDAAVPTWEQLENAMAVKT 384
 * QY 895 EGDQG-----LESLOGKDGYGFGSSQKLEGEEKQPT-PASSMP--QDQGIPPSLTOV 944
 * QY 385 VHGLVDFTIONYSRKGHETPOQPN-----SKYKTMSCDLRQOGGCPRGTNCTFAHS 436
 * QY 945 VH-----SAGRRIEVSPVPESEKRSKVFPPSETDTVAASTAQSPG----MNLISHS 991
 * QY 437 QEELEYKR---LRNKKI-----NATVRTRP----LNKVGVNNTVTITA-- 473
 * QY 992 ASSL1QQAFSELRLRAQMTEGPNTTAPNFSTHGTGFPVVPPFLSSIIAGVPTTAATAAPVP 1051
 * QY 474 -----GNVISVIGSSETTGKIVSSTINGISNAENS-----WSQLSI 508
 * QY 1052 ATSSPNDISTSVIQSEVT--VPEFEGIAGVATSTGVVTSGGGLIPPVSEPVSVS 1108
 * QY 509 RSTPSTLRALETVKVGKVGAN----GONAAGGSAD SVTENKIG---SPPKTPVSN 557
 * QY 1109 SITPAVSVSISTSSLOVFTSISIVSITALYVSVTSATSASSAGGSTATPPKPPAV 1168
 * QY 558 VAATSGPSNGVTELNSV-----POKSPSPFLTRVPUYVPPHSENIOYF 599
 * QY 1169 VSQQAGASTTGVATLTSVSTTQSPTASQSLQIQSSTSSTPIAETVVAHSILD-KTS 1227
 * Db 600 QDPRTQIFPEVQVQTGYVPPP---TVPGACPV_PRFVTSNNVFESSIPASMP 653
 * Db 1228 HSSTTGLAISL-SASSSSSPGAGCYSITSQPGGHLPLVPSVIASTPLQAMGPTSTP 1286
 * Qy 654 YADHYSFTSPRDRMMNNSSPYOPPPPOPYGPVPPVPSGM-----YAVVYDS 697
 * Db 1287 L-----LQVQPSIPLPVPUVANPAVQOQLIHQOPQALLPNPQPHTCPEVD 1334
 * Qy 698 RRIWIHPPMYQRDDI-----IRS--NSLPPMDVMSSV-YOTSLRERYNSLDGYVSA-- 746
 * Db 1335 DT--QPKAPGIDDKTILEEKURSLSEHSSSGAONHASVSLTSVTPGTTAVA 1392
 * Qy 747 -----CQPSE-PRTYPPREPC---GHLTKSCBQIRR-KPQWAQHTQKA 790
 * Qy 1393 PSKLUJSTSTCLPPNPLPGLTVALFVTPVTPGCGYSTPVSTTSGVVKPGT---APSKP 1448
 * Qy 791 PLVSS-TLPVATOSTPPSPSPLFSVDFRADSESVS GTKFEBDHLSHYSPWSCGTGSCIN 849
 * Db 1449 PLTKAPVLPQGTELP-----AGTIPS-E 1470
 * Qy 850 AIDSPPKDVITANSNATMJDPS-----GDKVKKRKHFLFETORRK--- 888
 * Db 1471 QLPPFPGPSPSLTQSQQPLEDIDAQLRRTLSPEXITVTSAVGPVSMAPTAITEAGTOPKG 1530
 * Qy 889 ----ERDPIIPTSDGGIISKWQ---ATSRSSRTGQHITDPVQATASOCASATRPIVS 938
 * Qy 1531 VSQVKEGPVLATSSGAGVKGGRPVSYAAGDAQGKNSKEDAKSVFHFSSTSSVSL 1590
 * Qy 939 DVVPVYNAV-----DSRMSSYGNFAT-SAHYTERDRFTVTDIS--G 977
 * Db 1591 SSSPESTLVKBPNGTIPGSSDVSESAHKTTASEAKSDTQGPKVGRFOVTTANKVG 1650
 * Qy 978 HRKHSSTGDLIS-----LELOQAKSNLILQOREANAJAMQOKNN----- 1016
 * Db 1651 RFSVSKMEKDITDKKKBGPVVASPPFEMDLEQAVLPAPIVKPKRKPSEPSHLLNGPSDPEA 1710
 * Qy 1017 ----SLDEGR--HILNLNLSKETBLRN-----GELOSQY-TEDATDITKDRIELEL 1061

RESULT 15
 US-09-854-856-16
 Sequence 16, Application US/09854856
 Patent No. 6541252
 GENERAL INFORMATION:
 APPLICANT: Walké, D. Wade
 APPLICANT: Hiblun, Erin
 APPLICANT: Donoho, Gregory
 APPLICANT: Turner, C. Alexander Jr.
 TITLE OF INVENTION: Human Kinases and Polynucleotides
 TITLE OF INVENTION: Encoding the Same
 FILE REFERENCE: LEX-0178-USA
 CURRENT APPLICATION NUMBER: US/09/854,856
 CURRENT FILING DATE: 2001-05-14
 PRIOR APPLICATION NUMBER: US 60/206,015
 PRIOR FILING DATE: 2000-05-19
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 16
 LENGTH: 1999
 TYPE: PRT
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1)..(1999)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-854-856-16

Query Match 3.1%; Score 193.5; DB 2; Length 199;
 Best Local Similarity 19.2%; Pred. No. 9.5e-06; Gaps 57;
 Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

Qy 114 CGKGVAYINGQSSALSPPMORKVLTUNQCVBEEGRV-AMHARAILGERTWTTELIOHQHON 172
 * Db 720 QOPSSSLTGTVSSQPOHQPOQGQIQTQATPQQTQVYQSLQTSSEATTAQPVQPA 779
 * Qy 173 POQLSANLWAARVARGCQFLCPA----MQEALKVVLUALBEDGSSLRSRKVLVFFVORL 227
 * Db 780 PQVLPQVSAGKQSTQGVSOPAEPVAVAOQPAOPTTASSVSDAHSID--VASGMSDG 836
 * Qy 228 EPRFOASKTSIGHVWOLYRASCVKTRKEDDSSIMQLK----EEFRSYEARREHD 281
 * Db 837 NENVESSSGRHEGRTRKHKRS--VRSRSRHEKTSRPKURILINVSNKGDRVCEOLETHN 895
 * Qy 282 AQVHIAEAGLRISPEQWSSLY-GDLAKSHMOSIDKLQSPSEFAKSVOELTIVLQR 340
 * Db 896 RKMVTFKFDLD-GDNPEETATMVNNDFILAIERESFVDQVRETEKADEMSEDSVVERP 954
 * Qy 341 TGDPAVLNRPHLELANDID-----PNPDAVSTWEQLENAMAVKT 384
 * Db 955 EGDQG-----LESLOGKDGYGFGSSQKLEGEEKQPIASSMP--QDQGIPPSLTOV 1004
 * Qy 385 VHGLVDFTIONYSRKGHETPOQPN-----SKYKTMSCDLRQOGCPRGTNCFAHS 436
 * Db 1005 VH-----SAGRRIEVSPVPESEKRSVFPSEITDTVAASTAQSPG----MNLISHS 1051
 * Qy 437 QEELEYKR---LRNKKI-----NATVRTRP----LNKVGVNNTVTITA-- 473

Db 1052 ASSLSLQQAFSELERRAQMTBGFNTAPPNFSHTGPTTPVPPFLSSIAVGPTAAATPVP 1111
 QY 474 -----GNVTSVIGSHETTGKIVPSTNGTISNAENS-----VSQOLIS 508
 Db 1112 ATSSPPNDISTSVILOSEVT--VPTIEGIAQWATSGVUTSGGLPPIPVSSESPVLSVVS 1168
 QY 509 RSTDSTURALSTVVKKGKVGAN-----GQNAAGPSAD-SVTEENKIG---SPPKTPVSN 557
 Db 1169 STIPAVVISITTSISLQVPTSTSETIVSSTALYPSVTSAASAGGSTATPGPKPAV 1228
 QY 558 VATTSKGPNSVGETHNSV-----POKSPFLTRUPVUPPHSENIOF 599
 Db 1229 VSQQAGAGSTTWGATLUSVSTTSEPSSTASQSLSIQLSSTSSTPLABTVWSAHSID-KTS 1287
 QY 600 QDPRTOIPFEVPPQYPOGYGYPYPPP-----TVPAGVAPCV-PRFVRSNNVBSSLPBPASMP 653
 Db 1347 L-----LPQVSPILPVQEVANPAVAQOPLIHQSOPQALPNOPHTHCPEVDS 1394
 QY 698 RNIWRPMWQDII-----IRS - NSLPMWDVMISSV-YOTSLERBNSLDGYISVA-- 746
 Db 1395 DT--QIKAPGIDDKIYLEEKURSLSEHSSGAQHASVUSLETSLVTESTVTPGIFTAVA 1452
 QY 747 -----COPRSE-BRTVPLRREPC--GHILKTSCEBIRR-KPDDWAQYHTOKA 790
 Db 1453 PSKLITSTTSTCUPPNULPIGTVALFTVTPGQVSTPSTTSGVKPGT--APSXP 1508
 QY 791 PLVSS-TLPVATQSPPPSPLFSVOPRADSESVSTKFEEBDHLHYSPPSCGTGSCIN 849
 Db 1509 PLTKAPVLPVGTELP-----AGTLPS--E 1530
 Qy 850 ALDSEKDVIANSNALMDS-----GDVKRVLHFETQRK--- 888
 Db 1531 QLPPPPGPSPSLTQSOCPLDQALRRTLSPEXITVSAVGPSMAPTAITEAGTOPKG 1590
 Qy 889 ---BEDPIIPFFSDGPILKSGW-----AISRRSRGHTDPVOATASOCSATKPIVS 938
 Db 1591 VSQVEGPVIATSSGAGVFRKGFRQVSAADGQAEKGKNSEDASVHFESSTSSSVS 1650
 Qy 939 DVYPVNAV-----DSRMSSYGMETS-SAHYVERDRFTVDIS--G 977
 Db 1651 SSPESTLVKEPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFOVTTANKVG 1710
 Qy 978 HRKASTGDL-----LELOQKNSLJLQBANALAMQKIN----- 1016
 Db 1711 RFFSVSKTEKDITDKKRGPVASPPENDQAVLPAVTKPKEKEPELSEPSHNGPSSDPEA 1770
 Qy 1017 ----SLDEGR--HILTNLISKETBLR-----GELOSDY-TEDATDTKPDIELEL 1061
 Db 1771 AFLSRDVDDSSGSPHOSKKSFSQNSLSNSFNNSMSDNESDIEDBKEL 1830
 Qy 1062 SALDTPEDGCOSEPERBILDQLOGSISONDOLN-----GMATEENGHVOQHKEPPK 1114
 Db 1831 RRL-----RDKHILKEIOPDLSRKRHEITSLYTKLGKVPAVILPPAIDLGRKRRPTK 1883
 Qy 1115 QK-----KOSLGEHR-----VILEEQTILPVTCISQPLVYSISACLP 1155
 Db 1884 SKGSKSKSRSSLIGNKSPQLSGNLGSOASAASVLPQOQTLHPGPN----IPBEGONQLLQP 1938
 Qy 1156 ITTSVSGNL 1165
 Db 1939 LKPSTSSDNL 1948

Search completed: May 24, 2005, 12:49:35
 Job time : 37 secs

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Db ; SEQ ID NO: 2
; LENGTH: 1191
; TYPE: PR_T
; ORGANISM: Homo sapiens
; US-10-619-992-2

Query Match 100.0%; Score 6215; DB 5; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Index 0; Gap 0;

Matches 1191; Conservative 0; MisMatches 0; Query 1 MPVQAAQWTERFLSCPCYCNEFDENYKPLSLGCSHTVKTCCLKJLRKACPPDQTAINTD 60
Db 1 MPVQAAQWTERFLSCPCYCNEFDENYKPLSLGCSHTVKTCCLKJLRKACPPDQTAINTD 60
Db 61 IDVLVPNFAFLQVLGAQVPHOSPKTSLNQENKHEVAKCCKVEDALYLAKPLSGKGKVAS 120
Db 11 LNQALSRSRMRKLUVTLNQNLVVEBGRVRMARAASLGERVTTELILOHONPOOLSNL 180
Db 61 IDVLVPNFAFLQVLGAQVPHOSPKTSLNQENKHEVAKCCKVEDALYLAKPLSGKGKVAS 120
Db 121 LNQALSRSRMRKLUVTLNQNLVVEBGRVRMARAASLGERVTTELILOHONPOOLSNL 180
Db 1121 LNQALSRSRMRKLUVTLNQNLVVEBGRVRMARAASLGERVTTELILOHONPOOLSNL 180
Db 181 WAAVRARGCQLGPAMQEBALKVULVLAEDSALSRSRKVULFVORLERPFPASKTSIG 240
Db 1811 WAAVRARGCQLGPAMQEBALKVULVLAEDSALSRSRKVULFVORLERPFPASKTSIG 240
Db 241 HVWQLIYRASCFKVTKRDESSLWOLKEFRSYEARRLRREDAQIVHIAQMAGLRSPEQW 300
Db 2411 HVWQLIYRASCFKVTKRDESSLWOLKEFRSYEARRLRREDAQIVHIAQMAGLRSPEQW 300
Db 301 SSLYCDLAHKSHMOSIDIKLQSPESFAKSVOELTIVLQRTGPANLNRLPHELLANI 360
Db 3011 SSLYCDLAHKSHMOSIDIKLQSPESFAKSVOELTIVLQRTGPANLNRLPHELLANI 360
Db 361 DPNPDAVSPTWEOLENAMAVKTVHGLVDIIONYSRKGHETPOQOPNSKYKTSQRDLR 420
Db 3611 DPNPDAVSPTWEOLENAMAVKTVHGLVDIIONYSRKGHETPOQOPNSKYKTSQRDLR 420
Db 36111 HVWQLIYRASCFKVTKRDESSLWOLKEFRSYEARRLRREDAQIVHIAQMAGLRSPEQW 300
Db 421 QOGCGCERGTNTFAISQBELYKJLENKKINATVRTFPPLINKGVNTVTAGNIVI 480
Db 4211 QOGCGCERGTNTFAISQBELYKJLENKKINATVRTFPPLINKGVNTVTAGNIVI 480
Db 4212 OOGCGFRGTTFAISQBELYKJLENKKINATVRTFPPLINKGVNTVTAGNIVI 480
Db 481 GSTETTGKIVESTNGISNAENSVSOLSRSTDSRTRALETVKVGKGANGQAGPSAD 540
Db 481 GSTETTGKIVESTNGISNAENSVSOLSRSTDSRTRALETVKVGKGANGQAGPSAD 540
Db 541 SVTENKIGSPPKTPVSNVAAATSAGSNVGTENSYQKSSFLTRPVYPYPHENIQFO 600
Db 541 SVTENKIGSPPKTPVSNVAAATSAGSNVGTENSYQKSSFLTRPVYPYPHENIQFO 600
Db 601 DPNPDAVSPTWEOLENAMAVKTVHGLVDIIONYSRKGHETPOQOPNSKYKTSQRDLR 420
Db 6011 DPNPDAVSPTWEOLENAMAVKTVHGLVDIIONYSRKGHETPOQOPNSKYKTSQRDLR 420
Db 661 FSPDRMNNSPYOPPPQPGVPPVPSGMAPVDSRRWPPMQRDDIRSNLPPM 720
Db 661 FSPDRMNNSPYOPPPQPGVPPVPSGMAPVDSRRWPPMQRDDIRSNLPPM 720
Db 721 DYNHSSVYQTSLRERYNLDGYSYVACQCPSEPRTTVPLPREPCGHLKTSCEBQRRKD 780
Db 721 DYNHSSVYQTSLRERYNLDGYSYVACQCPSEPRTTVPLPREPCGHLKTSCEBQRRKD 780
Db 781 QMAQHQTQAPLVSLPVATOSPPSPLESDVRFADFSVSQGKFEEDHLSHYSWMS 840
Db 781 QMAQHQTQAPLVSLPVATOSPPSPLESDVRFADFSVSQGKFEEDHLSHYSWMS 840
Db 841 CGTIGSCINAIDSEPKDVIANSNAVIMLDGDKVVRVLFETORTKEEPIIPSDGP 900
Db 841 CGTIGSCINAIDSEPKDVIANSNAVIMLDGDKVVRVLFETORTKEEPIIPSDGP 900
Db 901 IISKWGAISRSRRTGHTTDPOVATASQGATKPIVSVDYVYNAUDSRWSSYGEATS 960
Db 901 IISKWGAISRSRRTGHTTDPOVATASQGATKPIVSVDYVYNAUDSRWSSYGEATS 960
Db 961 SAHYVERDRFTTDLGSHKRKUSTGULSLQOAKNSNLQOREANALAMQKNSLDE 1020
Db 961 SAHYVERDRFTTDLGSHKRKUSTGULSLQOAKNSNLQOREANALAMQKNSLDE 1020
Db 961 SAHYVERDRFTTDLGSHKRKUSTGULSLQOAKNSNLQOREANALAMQKNSLDE 1020
Db 1021 GFRHTLNLSSKEIELRNGELOSSDYTEDATDIPRDIELESLADTDEPGCSEPEBIL 1080
Db 1021 GFRHTLNLSSKEIELRNGELOSSDYTEDATDIPRDIELESLADTDEPGCSEPEBIL 1080
Db 1081 DIOLGITSSQNDOQDINGMAVENGHQPVQHQKEPKPKQKQSLGDBHVILEBQKNTLPVTSFC 1140
Db 1081 DIOLGITSSQNDOQDINGMAVENGHQPVQHQKEPKPKQKQSLGDBHVILEBQKNTLPVTSFC 1140
Db 1141 SQQPLVYSISNACLPLITSVAGNLLKTHMSEKNDFLPKVANGKVN 1191
Db 1141 SQQPLVYSISNACLPLITSVAGNLLKTHMSEKNDFLPKVANGKVN 1191
Db 1141 SQQPLVYSISNACLPLITSVAGNLLKTHMSEKNDFLPKVANGKVN 1191
Db ; RESULT 2
; US-10-619-992-2
; Sequence 2, Application US/10619992
; Publication No. US2005039153A1
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a
FILE REFERENCE: 00-617-A
CURRENT APPLICATION NUMBER: US/10619, 992
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: US/09/921,099
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0

RESULT 3
US-09-921-099-4
; Sequence 4, Application US/09921099
; Patent No. US20020107372A1
; GENERAL INFORMATION:
; APPLICANT: Hefenrider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
FILE REFERENCE: 00-617-A
CURRENT APPLICATION NUMBER: US/09921,099
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 1191
TYPE: PRT
ORGANISM: Homo sapiens
US-09-921-099-4

Query Match, 99.9%; Score 6207; DB 3; Length 1191;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MIVYQQAQWTETLSLSPICYNEDTENVKPKISGCSHTVKCINKLKLRKACPPDTAINTD 60
Db 1 MAVQAQWTERFLSPICYNEDTENVKPKISLGCSTVCKTCINKLKLRKACPPDTAINTD 60

Qy 61 IDVLPINPVALQLVGAQPDHQSIKSLNIGENKHYEAKKVEDALYKLSGGKVAS 120
Db 61 IDVLPINPVALQLVGAQPDHQSIKSLNIGENKHYEAKKVEDALYKLSGGKVAS 120

Qy 121 LNQASALSRPMOKRVLTVNLNCOLVEERGRVRAMAARASLGERVTTEILQHONPOQLSANL 180
Db 121 LNQASALSRPMOKRVLTVNLNCOLVEERGRVRAMAARASLGERVTTEILQHONPOQLSANL 180

Qy 181 WAAVRARGCQTPGAMOBEALKVLAEDGALSRSKVLVFLVWRLEPRFOASKTSIG 240
Db 181 WAAVRARGCQTPGAMOBEALKVLAEDGALSRSKVLVFLVWRLEPRFOASKTSIG 240

Qy 241 HWVQLYRASECFKTRDEDSIMOLKEERSYEARREHQAMQHIAAMEAGRLSPEQW 300
Db 241 HWVQLYRASECFKTRDEDSIMOLKEERSYEARREHQAMQHIAAMEAGRLSPEQW 300

Qy 301 SLLYGLDAHKSHMOSIDIKQPSPEFAKSQBLITVLOQTD PANLNRPHLELLANT 360
Db 301 SLLYGLDAHKSHMOSIDIKQPSPEFAKSQBLITVLOQTD PANLNRPHLELLANT 360

Qy 361 DPNPDAVSPTMELQLENAMAVYKVWGVQDFTONYRKHETPQPOPNSKRTSMCRDLR 420
Db 361 DPNPDAVSPTMELQLENAMAVYKVWGVQDFTONYRKHETPQPOPNSKRTSMCRDLR 420

Qy 421 QOGGCGRGTNCFAHSQEELEYCYRLRKKINATVRFLPLKVGVNNTTAGNIVSI 480

RESULT 4
US-10-619-992-4
; Sequence 4, Application US/10619992
; Publication No. US20050239163A1
; GENERAL INFORMATION:
; APPLICANT: Hefenrider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene
FILE REFERENCE: 00-617-A
CURRENT APPLICATION NUMBER: US/10-619, 992
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: US/09/921, 099
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 1191
TYPE: PRT
ORGANISM: Homo sapiens
US-10-619-992-4

Db 421 QOGGCGRGTNCFAHSQEELEYCYRLRKKINATVRFLPLKVGVNNTTAGNIVSI 480
Qy 481 GSTETGKIVPSTNGISNAENVSQLSRSTSDSTRALETUVKKGKVGANGQANGPSAD 540
Db 481 GSTETGKIVPSTNGISNAENVSQLSRSTSDSTRALETUVKKGKVGANGQANGPSAD 540
Qy 541 SVTENKIGSPPKTPVSNAATSAGFSNVGBLNSVQKSSPFLTRPVYPHSENQYFQ 600
Db 541 SVTENKIGSPPKTPVSNAATSAGFSNVGBLNSVQKSSPFLTRPVYPHSENQYFQ 600
Qy 601 DPRTOPIFEVPOYPOGYYPGPPTVAGVACPVPFRVRNNVPESSLPPASMPYADYST 660
Db 601 DPRTOPIFEVPOYPOGYYPGPPTVAGVACPVPFRVRNNVPESSLPPASMPYADYST 660
Qy 661 FSPDRMNSSPYOPPPQPOQPVPPPGMAYPVDSRRIWRPPMQRDDITRNSLPPM 720
Db 661 FSPDRMNSSPYOPPPQPOQPVPPPGMAYPVDSRRIWRPPMQRDDITRNSLPPM 720
Db 721 DMHSSVYQTSLRERYNLDGYSVACQPSEPRTVPLPREPCGHILKTSCBQIRKP 780
Db 721 DMHSSVYQTSLRERYNLDGYSVACQPSEPRTVPLPREPCGHILKTSCBQIRKP 780
Qy 781 QWAQHPTQAKLVLSSLTPLVATQSPPPSPFSDVDRADFBESVSGTKFEECHLHSYSPWS 840
Db 781 QWAQHPTQAKLVLSSLTPLVATQSPPPSPFSDVDRADFBESVSGTKFEECHLHSYSPWS 840
Qy 841 CGTIGSCINAINADSEPKDVIANSNAVLMDLSDGVKRRVHFETQRTKEEDIPIPSPGP 900
Db 841 CGTIGSCINAINADSEPKDVIANSNAVLMDLSDGVKRRVHFETQRTKEEDIPIPSPGP 900
Qy 901 IISKWGAISRSRTGHTDVQATASQGSATKPSVSDYKPYVAVDSRWSYNEATS 960
Db 901 IISKWGAISRSRTGHTDVQATASQGSATKPSVSDYKPYVAVDSRWSYNEATS 960
Qy 961 SAHYVERDRFTDLSGRKHSSTGDLLSLQQAKNSLILQOREANALAMQKNSLDE 1020
Db 961 SAHYVERDRFTDLSGRKHSSTGDLLSLQQAKNSLILQOREANALAMQKNSLDE 1020
Qy 1021 GRHLTLNLSLKEIELRNGELOSDYTEDATDTPKDRDIELESLADPDEPQOSEPIEEL 1080
Db 1021 GRHLTLNLSLKEIELRNGELOSDYTEDATDTPKDRDIELESLADPDEPQOSEPIEEL 1080
Qy 1081 DIOLGISSQNDOLLNGMAVENGHPOQHKEPPKOKQSLGEDHVILEQKTIPLPTSCF 1140
Db 1081 DIOLGISSQNDOLLNGMAVENGHPOQHKEPPKOKQSLGEDHVILEQKTIPLPTSCF 1140
Qy 1141 SQPLVVISNASCLPITTSVAGNLILKTHVMSEDKNDFLKPVANGKVN 1191
Db 1141 SQPLVVISNASCLPITTSVAGNLILKTHVMSEDKNDFLKPVANGKVN 1191

Query Match 99.9%; Score 6207; DB 5; Length 1191;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1190; Conservative 0;

Qy 1 MPVOAQWTERLSPCIPYNEFEDENVKPISIGCSHTVCKTCILNKLRKACCPFDQINTD 60
 1 MAVOAKQWTERLSPCIPYNEFEDENVKPISIGCSHTVCKTCILNKLRKACCPFDQINTD 60
 61 IDVLPNFALLQVGAQVPHOSIKUSNLGENKHVEAKCVEDALYKPLSGKGVAS 120
 61 IDVLPNFALLQVGAQVPHOSIKUSNLGENKHVEAKCVEDALYKPLSGKGVAS 120

Qy 121 LNQSAISRPMKRKLVLVNCOLVCEEEGRVRAMARSLGERVTTELQHNPQISANL 180
 121 LNQSAISRPMKRKLVLVNCOLVCEEEGRVRAMARSLGERVTTELQHNPQISANL 180

Qy 181 WAVRARGCQFLGPMAMOEALKVLVLAEDSALSRLKVLVFLVORLEPREQASKTIG 240
 181 WAVRARGCQFLGPMAMOEALKVLVLAEDSALSRLKVLVFLVORLEPREQASKTIG 240

Qy 241 HVVQLIYRASECPKVTRDEDSIMLQKEEFSYEALRREHDQIVHIAEGLRSPEQW 300
 241 HVVQLIYRASECPKVTRDEDSIMLQKEEFSYEALRREHDQIVHIAEGLRSPEQW 300

Qy 301 SSSLYGDLAHKSHMOSIDKQSPESAKSYQBLTIVLORTGPANLNRLRPHLEJANI 360
 301 SSSLYGDLAHKSHMOSIDKQSPESAKSYQBLTIVLORTGPANLNRLRPHLEJANI 360

Qy 361 DNPDAVSPTEOLENAWMVAKTVVHGLDFQIVNSRKGHETPOOPNSKTKSMCRDLR 420
 361 DNPDAVSPTEOLENAWMVAKTVVHGLDFQIVNSRKGHETPOOPNSKTKSMCRDLR 420

Qy 421 QGGCPRGTCTFAHSOELLYKRLANKKINATVRTPLLNKGVNTVTAGNIVSI 480
 421 QGGCPRGTCTFAHSOELLYKRLANKKINATVRTPLLNKGVNTVTAGNIVSI 480

Db 481 GSTETTGKIVSTNGSNAENSVSOLISRSTDTRALETWVKVGANGCONAGPSAD 540
 481 GSTETTGKIVSTNGSNAENSVSOLISRSTDTRALETWVKVGANGCONAGPSAD 540

Qy 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTELNSVQKSSFLTRPVYPVPPRENTQFQ 600
 541 SVTENKIGSPPKTPVSNVAATSAGPSNGVTELNSVQKSSFLTRPVYPVPPRENTQFQ 600

Db 601 DPTQIPFEVQYQPGTYPPPTVAGVACQCPYPRFRSNNPWELLPPASMPYADYST 660
 601 DPTQIPFEVQYQPGTYPPPTVAGVACQCPYPRFRSNNPWELLPPASMPYADYST 660

Db 601 DPTQIPFEVQYQPGTYPPPTVAGVACQCPYPRFRSNNPWELLPPASMPYADYST 660
 601 DPTQIPFEVQYQPGTYPPPTVAGVACQCPYPRFRSNNPWELLPPASMPYADYST 660

Qy 661 FSPRDRMNSSPYQPPPQPKGPPVPPSGMAYPAVYDRIWPPMQRDDITRNSLPPM 720
 661 FSPRDRMNSSPYQPPPQPKGPPVPPSGMAYPAVYDRIWPPMQRDDITRNSLPPM 720

Db 721 DMHSSVYQTTERVNLDGJYVAQQPPEBPRTTVPLPPRCGHLKTSEQRKPD 780
 721 DMHSSVYQTTERVNLDGJYVAQQPPEBPRTTVPLPPRCGHLKTSEQRKPD 780

Db 781 QWAOYHOKAPVSVTLPVATQSPTPSPLSVDFRDSFSVSGTKFPEELHRYSPWS 840
 781 QWAOYHOKAPVSVTLPVATQSPTPSPLSVDFRDSFSVSGTKFPEELHRYSPWS 840

Db 840 CCGTGSINAIDSRPKVIANSAVMDLSDGDKRVRHLEFETORRTKEEDPIIPPSDG 900
 841 CCGTGSINAIDSRPKVIANSAVMDLSDGDKRVRHLEFETORRTKEEDPIIPPSDG 900

Db 900 IISKWGMASRSRTGYWTDPOQATASQGSAKTPKISVSDYVYVNAVDRSNSYGBEAT 960
 901 IISKWGMASRSRTGYWTDPOQATASQGSAKTPKISVSDYVYVNAVDRSNSYGBEAT 960

Qy 961 SAHYVERDRFTIDSLSGRKHSTGDSLSELOQAKNSLJQREANALAMOKWNISIDE 1020
 961 SAHYVERDRFTIDSLSGRKHSTGDSLSELOQAKNSLJQREANALAMOKWNISIDE 1020

Db 961 SHYVERDRFTIDSLSGRKHSTGDSLSELOQAKNSLJQREANALAMOKWNISIDE 1020
 961 SHYVERDRFTIDSLSGRKHSTGDSLSELOQAKNSLJQREANALAMOKWNISIDE 1020

Qy 1021 GRHTLNLISKEIELRNGELOSDTEDTTPKPDIEBSALDTDEPGQSEPEIIL 1080
 1021 GRHTLNLISKEIELRNGELOSDTEDTTPKPDIEBSALDTDEPGQSEPEIIL 1080

Db 1081 DIOLGISSQNDQOLLNGMAVENGHPYQOHQKEPPKOKKQKSIGEDHYLEOKTILPUTSCF 1140
 1081 DIOLGISSQNDQOLLNGMAVENGHPYQOHQKEPPKOKKQKSIGEDHYLEOKTILPUTSCF 1140

Qy 1141 SQPLVYSISNASCLPITTYSAGNLITKHMNSEDKNDFLKPVANGKMNS 1191
 1141 SQPLVYSISNASCLPITTYSAGNLITKHMNSEDKNDFLKPVANGKMNS 1191

Db 1141 SQPLVYSISNASCLPITTYSAGNLITKHMNSEDKNDFLKPVANGKMNS 1191

RESULT 5
 US-10-485-225-8
 ; Sequence 8, Application US/10485225
 ; Publication No. US20050181355A1

; GENERAL INFORMATION:

APPLICANT: Greener, Tsvika
 APPLICANT: Moskowitz, Haim
 APPLICANT: Reiss, Yuval
 APPLICANT: Alroy, Iris

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 FILE REFERENCE: PROL-P02-001
 CURRENT APPLICATION NUMBER: US/10/485, 225
 CURRENT FILING DATE: 2004-01-30
 PRIORITY APPLICATION NUMBER: US 60/308, 958
 PRIORITY FILING DATE: 2001-07-31
 PRIORITY APPLICATION NUMBER: US 60/345, 846
 PRIORITY FILING DATE: 2001-11-09
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 1048
 TYPE: PRT

; ORGANISM: Homo sapiens

US-10-485-225-8

Query Match 88.2%; Score 5483; DB 5; Length 1048;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1048; Conservative 0;

Qy 1 MPVOAQWTERLSPCIPYNEFEDENVKPISIGCSHTVCKTCILNKLRKACCPFDQINTD 60
 1 MPVOAQWTERLSPCIPYNEFEDENVKPISIGCSHTVCKTCILNKLRKACCPFDQINTD 60

Db 121 LNQSAISRPMKRKLVLVNCOLVCEEEGRVRAMARSLGERVTTELQHNPQISANL 180
 121 LNQSAISRPMKRKLVLVNCOLVCEEEGRVRAMARSLGERVTTELQHNPQISANL 180

Qy 121 IDVLPNFALLQVGAQVPHOSIKUSNLGENKHVEAKCVEDALYKPLSGKGVAS 120
 121 IDVLPNFALLQVGAQVPHOSIKUSNLGENKHVEAKCVEDALYKPLSGKGVAS 120

Db 181 WAVRARGCQFLGPMAMOEALKVLVLAEDSALSRLKVLVFLVORLEPREQASKTIG 240
 181 WAVRARGCQFLGPMAMOEALKVLVLAEDSALSRLKVLVFLVORLEPREQASKTIG 240

Qy 241 HVVQLIYRASECPKVTRDEDSIMLQKEEFSYEALRREHDQIVHIAEGLRSPEQW 300
 241 HVVQLIYRASECPKVTRDEDSIMLQKEEFSYEALRREHDQIVHIAEGLRSPEQW 300

Db 301 SSSLYGDLAHKSHMOSIDKQSPESAKSYQBLTIVLORTGPANLNRLRPHLEJANI 360
 301 SSSLYGDLAHKSHMOSIDKQSPESAKSYQBLTIVLORTGPANLNRLRPHLEJANI 360

Db 360 IISKWGMASRSRTGYWTDPOQATASQGSAKTPKISVSDYVYVNAVDRSNSYGBEAT 360
 361 DNPDAVSPTEOLENAWMVAKTVVHGLDFQIVNSRKGHETPOOPNSKTKSMCRDLR 420
 361 DNPDAVSPTEOLENAWMVAKTVVHGLDFQIVNSRKGHETPOOPNSKTKSMCRDLR 420

Qy 421 QGGCPRGTCTFAHSOELLYKRLANKKINATVRTPLLNKGVNTVTAGNIVSI 480
 421 QGGCPRGTCTFAHSOELLYKRLANKKINATVRTPLLNKGVNTVTAGNIVSI 480

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 24915
; LENGTH: 819
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-11-097-143-24915

Query Match 24.7%; Score 1538; DB 6; Length 819;
Best Local Similarity 40.5%; Pred. No. 2.1e-97; Mismatches 226; Indels 242; Gaps 29;
Matches 386; Conservative 98; Mismatches 226; Indels 242; Gaps 29;

Qy ||||| 541 SVTENKIGSPPKTPVSNVATSAAGPSNVGTELNSVQKSSPFLTRVYVPPHSENQYFO 600
Db 541 SVTENKIGSPPKTPVSNVATSAAGPSNVGTELNSVQKSSPFLTRVYVPPHSENQYFO 600
; 481 GSTETGKIVPSTNGISNAENSVSOLSRSTSTDSTRALETVKVKVGANGQNAAGPSAD 540
; 601 DPRTOFPFEVQYQPOGYPPPTVAGACVCPVRVSNNPESLPPASMPYDHYST 660
Db 601 DPRTOFPFEVQYQPOGYPPPTVAGACVCPVRVSNNPESLPPASMPYDHYST 660
; 661 FSPDRMNSSPYQPPPQPKCVPVPPVPSGMVAPVIDSRRWPPWMQRDDIRSLSPM 720
Db 661 FSPDRMNSSPYQPPPQPKCVPVPPVPSGMVAPVIDSRRWPPWMQRDDIRSLSPM 720
; 661 FSPDRMNSSPYQPPPQPKCVPVPPVPSGMVAPVIDSRRWPPWMQRDDIRSLSPM 720
Qy ||||| 721 DMHSSVYQTSRERYNLDGIVSYACQPPSEPRTRVPLPREPCGHILKTSCBQIRKPD 780
Db 721 DMHSSVYQTSRERYNLDGIVSYACQPPSEPRTRVPLPREPCGHILKTSCBQIRKPD 780
; 781 QWAQYHTQAKPLVSSTLPVATOSPTPSPFLPSVDEADESSVSCTKFEEDHLSTYSPWS 840
Db 781 QWAQYHTQAKPLVSSTLPVATOSPTPSPFLPSVDEADESSVSCTKFEEDHLSTYSPWS 840
; 781 QWAQYHTQAKPLVSSTLPVATOSPTPSPFLPSVDEADESSVSCTKFEEDHLSTYSPWS 840
Qy ||||| 781 QWAQYHTQAKPLVSSTLPVATOSPTPSPFLPSVDEADESSVSCTKFEEDHLSTYSPWS 840
; 841 CGTIGSCINAIDSEPKDVIANSNAVJMDSGDVKRVHLFETQRKEEDPIIPSDGP 900
Db 841 CGTIGSCINAIDSEPKDVIANSNAVJMDSGDVKRVHLFETQRKEEDPIIPSDGP 900
; 841 CGTIGSCINAIDSEPKDVIANSNAVJMDSGDVKRVHLFETQRKEEDPIIPSDGP 900
Qy ||||| 901 IISKGWAISSRTGHTDPVQATASQSATKPSVSDVYVNAVDMSRWSYNEATS 960
Db 901 IISKGWAISSRTGHTDPVQATASQSATKPSVSDVYVNAVDMSRWSYNEATS 960
; 901 IISKGWAISSRTGHTDPVQATASQSATKPSVSDVYVNAVDMSRWSYNEATS 960
Qy ||||| 961 SAHYVERDRFTVTDLSGRHKRKSSTGDLSTIQAQSNSLLOREANALANQOKNSLDE 1020
Db 961 SAHYVERDRFTVTDLSGRHKRKSSTGDLSTIQAQSNSLLOREANALANQOKNSLDE 1020
; 961 SAHYVERDRFTVTDLSGRHKRKSSTGDLSTIQAQSNSLLOREANALANQOKNSLDE 1020
Qy ||||| 1021 GRHLTNLNLSEKIELNGLDOSYTEDA 1048
Db 1021 GRHLTNLNLSEKIELNGLDOSYTEDA 1048
; 1021 GRHLTNLNLSEKIELNGLDOSYTEDA 1048

RESULT 6
US-11-097-143-24915
; Sequence 24915, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEAR ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

Qy ||||| 456 VNNTVTUTAGNIVSIVGSTETTGKIVPSTNGISNAENSVSOLSRSTSTDSTRALETVKVKV
Db 456 -----
; 525 GKVANGQNAAGPSADSVTENKIGSPPKTPVSNVATSAAGPSNVGTELNSP-OKSSPP 582
Db 525 GKVANGQNAAGPSADSVTENKIGSPPKTPVSNVATSAAGPSNVGTELNSP-OKSSPP 582
; 583 LTRVPPYPPHSEBNIQFOODPRTOQIPFEPVQFOTGTYPPPTVAGACVCPVRVSNN
Db 583 LTRVPPYPPHSEBNIQFOODPRTOQIPFEPVQFOTGTYPPPTVAGACVCPVRVSNN 642
; 488 LGNRPMLPMSP-MHMGSPP-----
Db 488 LGNRPMLPMSP-MHMGSPP-----
; 488 LGNRPMLPMSP-MHMGSPP-----
; 488 LGNRPMLPMSP-MHMGSPP-----
Db 488 LGNRPMLPMSP-MHMGSPP-----
; 522 GLD1SP-----GGGL 522
Qy ||||| 583 PESSLPAS--MP-YADHSTF--SPDRMNSSSPYQPPPQPYGVPPVPSGMVAP 694
Db 583 PESSLPAS--MP-YADHSTF--SPDRMNSSSPYQPPPQPYGVPPVPSGMVAP 694
; 523 PPSHHSPTRLIVPSRDSRFSGFGGGTPR-----
Db 523 PPSHHSPTRLIVPSRDSRFSGFGGGTPR-----
; 566 1PSPREQANPVAP-----
Db 566 1PSPREQANPVAP-----
; 695 YDSRRWPPMQRDDIRSLSPM--DINHSSVYQTSRERVNLDGYSVACOPP- 750
Db 695 YDSRRWPPMQRDDIRSLSPM--DINHSSVYQTSRERVNLDGYSVACOPP- 750
; 643 PESSLPAS--MP-YADHSTF--SPDRMNSSSPYQPPPQPYGVPPVPSGMVAP 694
Db 643 PESSLPAS--MP-YADHSTF--SPDRMNSSSPYQPPPQPYGVPPVPSGMVAP 694
; 567 --TORNANPPNFSVNLSNHKGMLPASGGDVPHLA-----NPWEQAVLAQQHHPP 614
Db 567 --TORNANPPNFSVNLSNHKGMLPASGGDVPHLA-----NPWEQAVLAQQHHPP 614
; 751 ----SEPRTRVPLPRECGHILKTSCBQIRRKDPAQHTQAKPLVS-STLPVATOS 803
Db 751 ----SEPRTRVPLPRECGHILKTSCBQIRRKDPAQHTQAKPLVS-STLPVATOS 803
; 615 OHQDQDQPSKPNPSPRLPLSLTUPATEDSFEEKKPBNVSIDLRPVEVNDAPLFRS 674
Db 615 OHQDQDQPSKPNPSPRLPLSLTUPATEDSFEEKKPBNVSIDLRPVEVNDAPLFRS 674
; 804 PTPPSPLFSVDFRADFSESVAGTKFEEDHLSHYSPNSCCGTTGICINAIDSPKDVIANS 863
Db 804 PTPPSPLFSVDFRADFSESVAGTKFEEDHLSHYSPNSCCGTTGICINAIDSPKDVIANS 863
; 675 -----NNNNNNNNNNNNNNNNHGSLLFN-NNGKDSANFVRS--DSTLDD 720
Db 675 -----NNNNNNNNNNNNNNHGSLLFN-NNGKDSANFVRS--DSTLDD 720
; 864 AVLMDLSDGDYKRRVLFETORRTKEBDPITPPSDGPIISKWGTATRSRSRTG 915
Db 864 AVLMDLSDGDYKRRVLFETORRTKEBDPITPPSDGPIISKWGTATRSRSRTG 915

RESULT 9

; Sequence 3665, Application US/11072512

; Publication No. US20060129945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHI, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUTKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKI, ICHIRO

; APPLICANT: SEKI, NAORIKO

; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTORYUKI

; APPLICANT: NAGHARI, KENJI

; APPLICANT: MASURO, YASUHIKO

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: 084325-0191

CURRENT APPLICATION NUMBER: US/11/072,512

CURRENT FILING DATE: 2005-03-07

PRIOR APPLICATION NUMBER: US 6/0350,978

PRIOR FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: JP 2001-379298

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3665

LENGTH: 522

TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-072-512-3665

Query Match 9.8%; Score 611; DB 6; length 522;

Best Local Similarity 34.1%; Pred. No. 2.3e-33; Mismatches 187; Conservative 76; Indels 98; Gaps 27;

Matches 187; Conservatve 76; Mismatches 187; Indels 98; Gaps 27;

QY 618 YPPPPTPVAGVAPCPVFRVRSNNPESLPPASPMYADHYSFSPRDRMNNSPQQPPP 677

Db 2 YYTPPP-----QCVSFYR----DPPSAPAPPAPEYLDPYI-QERVNNSQGTQO 49

QY 678 QPYGPPPPVPSGGMYAPVYDSRRIWRPPMYYORDITRSNLPPMDVMHSSV--YQTSRLR 735

Db 50 Q---YPP-----YPSHYDGRKRVIPAPSYTREIFRESPI-PIEPPAAVPSYFESRER 100

QY 736 YNSLDCCYYSVACQP---PS---EERTTVPLPRECGHHIKTSCEQRIRKPQDAQYHT 787

Db 101 YQQIESYYPVAPHRPTOIRPSYRKEPPYSLRPPQ---HPSLDBLRRKKEIMOLEE 156

QY 788 OKAPLVSTLRAVATOSPTPESPLFSVDFRADPSESVSGTKFEEEDHLHSYSPWCGTGSC 847

Db 157 RK---VISPPFA-PSPLP-FTRHEEEFDEDLKAG-KYKGNDYQSOPSPCOTIGS 210

QY 906 GALSSRSRTGHTTDVQATASQSATKPSVSDVYPPWADSWW--SSGG--HEATSS 961

Db 848 INNAIDSEPKDVJANSNAVLMDISGDGKVRRVHLFFETRRTKE--EDPITIPSDGILISKW 905

Db 211 IGTKOKAKPKDVWAAGSVMMVNEVKSM--RDQDLQRRAEATSPDDLIPGDRPTVSRF 268

QY 962 AHYVERDRFTVTLDSHRK--HSSGDLISLEHQ-----AKSNELLOR 1004

Db 327 GHPSBEERISMEVASHGKPLRSABEROLFLQQLNHOISQOTOLRGPEAVSNLVR 386

RESULT 10

; Sequence 1346, Application US/09867550

; Patent No. US20020082206A1

; GENERAL INFORMATION:

; APPLICANT: Leach, Martin D.

; APPLICANT: Mehraban, Fuad,

; APPLICANT: Conley, Pamela

; APPLICANT: Law, Debbie

; APPLICANT: Topper, James

; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and i

; TITLE OF INVENTION: Thereby

; FILE REFERENCE: 21402-013 (Curia-313)

CURRENT APPLICATION NUMBER: US/09/867,550

CURRENT FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: USN 60/208,427

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 2125

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1346

LENGTH: 95

TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-867-550-1346

Query Match 7.9%; Score 490; DB 3; length 95;

Best Local Similarity 100.0%; Pred. No. 4.1e-26; Mismatches 0; Indels 0; Gaps 0;

Matches 95; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

QY 1097 MAVENGHPVOQHKEPPKQKQKSIGEDHIVLEQKTIPLPTCSFQSPLYVSIASCLPI 1156

Db 1 MAVENGHPVOQHKEPPKQKQKSIGEDHIVLEQKTIPLPTCSFQSPLYVSIASCLPI 60

QY 1157 TTSAZGNLILKTHMSBENDFLKVEANGKNN 1191

Db 61 TTSAZGNLILKTHMSBENDFLKVEANGKNN 95

RESULT 11

; Sequence 48290, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Weisheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-03-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Autamax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 49290
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: DOMAIN
; NAME/KEY: DOMAIN
; LOCATION: (171)..(201)
; OTHER INFORMATION: Zinc finger, C3HC4 type (RING finger) domain identified by eMATRIX, OTHER INFORMATION: accession number BL00709B, p-value=5.313e-28, raw score of 21.58
; FEATURE: DOMAIN
; NAME/KEY: DOMAIN
; LOCATION: (171)..(201)
; OTHER INFORMATION: Zinc finger, C3HC4 type (RING finger) domain identified by eMATRIX, OTHER INFORMATION: accession number BL00709B, p-value=5.313e-28, raw score of 21.58
; OTHER INFORMATION: pram, accession name zf-C3HC4, E-value=0.014, PFam score of 12.6
; US-10-450-763-41493
; Query Match 4.3%; Score 267; DB 5; Length 276;
; Best Local Similarity 59.8%; Pred. No. 6.5e-10; Indels 16; Gaps 2;
; Matches 52; Conservative 9; Mismatches 10; Indels 16; Gaps 2;
; Qy 8 WTEFLSCPCICYNEFDENVKRISLGSHSTVCKTCLNKLHKAQCPFDQTAINTDIDULPVN 67
; Db 168 WT-----FDTPIRKISLGCGHTVCKMCLNKLHKAQCPFDQTTINTDIELLPVN 216
; Qy 68 FALLOLVGAQVFDHQSIKLSNLGENKH 94
; Db 217 SALLOLVGA----QALKITKILTDIH 238
; RESULT 13
; US-10-330-773-941
; Sequence 941, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 941
; LENGTH: 1552
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-330-773-941
; Query Match 3.3%; Score 208; DB 5; length 1552;
; Best Local Similarity 22.0%; Pred. No. 0.00012; Indels 252; Gaps 36;
; Matches 148; Conservative 82; Mismatches 190; Indels 252; Gaps 36;
; Qy 572 LNSVPDKSPRLTRPVVPPH-----SENTOYFQDPPTQTQIPPEVROYPQ---TGYVPP 621
; Db 1 MNSQPOQRSPRSPQRPOQQPRATIPNSPSR-----PQAQPTAVQANQHIMMVNHLPM 56
; RESULT 12
; US-10-450-763-41493
; Sequence 41493, Application US/10450763
; Publication No. US2005019675A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP2/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/00631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 41493
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: DOMAIN
; NAME/KEY: DOMAIN
; LOCATION: (63)..(105)
; OTHER INFORMATION: Ribosomal protein L30e proteins domain identified by eMATRIX, OTHER INFORMATION: accession number BL00709B, p-value=5.313e-28, raw score of 21.58
; FEATURE: DOMAIN
; NAME/KEY: DOMAIN
; LOCATION: (171)..(201)
; OTHER INFORMATION: Zinc finger, C3HC4 type (RING finger) domain identified by eMATRIX, OTHER INFORMATION: accession number BL00709B, p-value=5.313e-28, raw score of 21.58
; FEATURE: DOMAIN
; NAME/KEY: DOMAIN
; LOCATION: (171)..(201)
; OTHER INFORMATION: Zinc finger, C3HC4 type (RING finger) domain identified by eMATRIX, OTHER INFORMATION: accession number BL00709B, p-value=5.313e-28, raw score of 21.58
; OTHER INFORMATION: pram, accession name zf-C3HC4, E-value=0.014, PFam score of 12.6
; US-10-450-763-41493
; Query Match 4.3%; Score 267; DB 5; Length 276;
; Best Local Similarity 59.8%; Pred. No. 6.5e-10; Indels 16; Gaps 2;
; Matches 52; Conservative 9; Mismatches 10; Indels 16; Gaps 2;
; Qy 8 WTEFLSCPCICYNEFDENVKRISLGSHSTVCKTCLNKLHKAQCPFDQTAINTDIDULPVN 67
; Db 168 WT-----FDTPIRKISLGCGHTVCKMCLNKLHKAQCPFDQTTINTDIELLPVN 216
; Qy 68 FALLOLVGAQVFDHQSIKLSNLGENKH 94
; Db 217 SALLOLVGA----QALKITKILTDIH 238
; RESULT 13
; US-10-330-773-941
; Sequence 941, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 941
; LENGTH: 1552
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-330-773-941
; Query Match 3.3%; Score 208; DB 5; length 1552;
; Best Local Similarity 22.0%; Pred. No. 0.00012; Indels 252; Gaps 36;
; Matches 148; Conservative 82; Mismatches 190; Indels 252; Gaps 36;
; Qy 622 PPTVAGVAPCVPRVFSNVNPESLPPASPYADHYSTSPPDRMNNSPVQPPPQPYG 681
; Db 57 PYVPVOCPOYCIQYRHG-----PYYVSPQOY-----PVQPGPGPFY 96
; Qy 682 PVP--PPSGNATPYDSRRIWRPPWYQODDIIRNSLPPMDVMHSSVYQTSLRVRYN 738
; Db 97 PEGPGDFPNAYGTPVPSQ-----PVYQSAPI-----VPTQO-----130
; Qy 739 LDGYYSVACQPPSEPRPTVPLPREPCGHKLTSCEEQIR-RKDQWAOYHTOKAPLYSS-- 795
; Db 131 -----QPP-----PAKRE-----KKIRRPNQGSKDITEB--IMSGGG 163
; Qy 796 ---TLPVA--TQSPTPPSPLFSVDRFDESRSVSQSGTKFEDHLSHVSPWSCGTIGSCCN 849
; Db 164 SRNPTPPIGRPRSTPTPPQQLPSQ--VPEHSPVYGT--VESAHLAASTPVTA----- 212
; Qy 850 AIDS-----EPKDVIAINSNAVLMDLSDGDVGRVHLFETQRTRKBDPIIFSDGPRIS 903

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Db 213 ASDQKOBEPKPKDPVLSKSPSPVPLVLISGKK-----EQGQTSETTATVIAELPLPP 266
 Qy 904 KGAISRSRIGYHTDPVQATASQSATKISVSDVPMVYNAVDSRWS-----' 952
 Db 267 SPTTVSSVARS-----TIAPTSALSSQPI-----FTTAIDRCLESPRETIPI 313
 Qy 953 --SYGNBEATSSAHYVERDRFT-----' 988
 Db 314 PSLTSCETSDLPTNENDDDICKKPCSVAPNDIPLVSSTNLININGVSBKLATESIV 373
 Qy 989 SIELOQAKNSNLQOBAN-----' 1025
 Db 374 EIVKQEVL-----PITLEBINPPEMKLFIVPAATTVVSSPSAATVORVBLE-DESRTE 430
 Qy 1026 LNLISKEIELRNGLQED-YFEDATD-----' 1055
 Db 431 LSDAKEIQ-NKIEVEADQPEFELSQNLNSRRSPVPAQIAITVPTWKPKDRRTTE 489
 Qy 1056 --DIEELSAADTDEPDGQSBPIEELDIOQGISSONDQLINGMAVENGHIPVQOKEP 1112
 Db 490 EMLEASBLELKA-----EEBLSIDKVLESSEQDKWQGF----HP---ERDP 527
 Qy 1113 PKQKGOSLGEH 1124
 Db 528 SDLKVKVAVEEN 539

RESULT 14
 US-10-840-512-196
 ; Sequence 196, Application US/10840512
 ; Publication No. US20050125852A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CAENEPEL, SEAN
 ; APPLICANT: MANNING, GERRARD
 ; APPLICANT: CHARITCZAK, GLEN
 ; APPLICANT: GRIGORIEV, IGOR
 ; TITLE OF INVENTION: NOVEL KINASES
 ; FILE REFERENCE: 034536-1455
 ; CURRENT APPLICATION NUMBER: US/10/840,512
 ; CURRENT FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: 60/469,014
 ; PRIOR FILING DATE: 2003-05-09
 ; NUMBER OF SEQ ID NOS: 239
 ; SOFTWARE: PatentIn version 3.2
 ; LENGTH: 2377
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-840-512-196

Query Match 3.3%; Score 207; DB 5; Length 2377;
 Best Local Similarity 19.3%; Pred. No. 0.002%;
 Matches 216; Conservative 152; Mismatches 424; Indels 326; Gaps 46;

Qy 48 KCPFDQTAINT-----DIDVLPVNFAILQVGAQVDPHOSIKLNSLGEN 92
 Db 375 KRAFAKSVIGTPERMAPEMEEVKYEDVYAFGMCMLEMTSEV----- 421

Qy 93 KHYEVAKKCVEDALAYKPLSGGGKVASYLNGSL-----SRPMQRKLYTLV 139
 Db 422 -----YSECOMAQIIRRVTGSKV-PASFDKVAIPEVKELIEGCIRQNKRYSKDLN 475
 Qy 140 CQOLVEBRGRVAMRAARSLSLGRRTVTEULOHONPQLSANIWAVERGQFLGAMQEE 199
 Db 476 HAFFOETGVRLVLAFFDDGGERKIAKWLRLBDIKLK-----' 520
 Qy 200 ALKLVLLALEDOSALSRKVLVFLVQRLPREPQASKTSIGHVQ-----LLYRAS 250
 Db 521 AIEF-----SFDLRDVPAVDAENVESWYCEGDHKTMKAIDRVS 563
 Qy 251 CFWVTKRDEDDSSLMQKKEFRSAYEALREHDQVHITAMEAGLRISPEQMSSLLYKDLH 310
 Db 564 LIK-RKERRQOLVREEOFKRKOEESSTKQONEQQASVS-QAGI---QQLSAASTGPIA 617

RESULT 15
 US-11-096-568A-27756
 ; Sequence 27756, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alandov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 27756
 ; LENGTH: 674
 ; TYPE: PRT

Qy 311 KSHMOSIIKDQLOSPESFAKSVOBLTIVLQRIGDPANLRPHLELAVNIDPNPPDAVPT 370
 Db 618 PATSASVSTOPEPEPEADQHO-----LQYQOPSIISL-----DGTIBSGQS 662
 Qy 371 WEOLENAMVAIKTVHGLVDFIONVSRKGHT-----POPOQRIKYSMCRD 418
 Db 663 SVFTBSRVSQQTGSY-----SGBQAMSTGTAPGTVSSIQAOSQPHGIVVPESSMAQ 716
 Qy 419 LRQGCGCPRGNTCTFAHSQELEYKVRLNKKINATVTFPLUN-KVGVANNTVTTAGNV 476
 Db 717 GONOOGO-PSSSLACVISQ-----PIQHOOQGIQT----- 747
 Db 747 ISVIGSTETTGKIVPSTNGTSNAENSVSQIISRSTDSTLAETVKGKYGANGSONAG 536
 Db 748 -----VPSQQAV---QNSLPLQOASS-----EG 767
 Qy 537 PSADSTENKGSPPKTPVSNVAASAGPSN-VTELNSVPOKSSPFLTRPVPHSE 594
 Db 768 TTAQPSQSPQVAGTOLPVSOTVATQEGEPHIPVSTQPSVPUVHSGAHEMGOPILPTSL 827
 Qy 595 NIQYFODPRTRQIPFEVPOQ--POTGYVPPPTVACVACPVCPVFRVSNNVPESSLPASM 652
 Db 828 LPQY--PVSCIPISPVHSTRAOTESSVPTMAGINO--PLITLASATASSPGSP 882
 Qy 653 PYADHRYST-FSPRDRMSY-----OPPPPOPYGPV-----PVPSA-MYARVYD 696
 Db 883 VVPNQLPLTLLQVNPQLQSQVHQPLQLOPPTVOSIG-IPANLGQAAEGLPSPGDVLRQG-FP 940
 Qy 697 SRRIKRPMPQDDIRNSLRPMQHSSY-QTSLREYNSLOGYYSYACQPSEPERT 755
 Db 941 SR--LPPQYQPGDSNITAPSNSVASYCISTVLAAPPSPMTEALATOCYPPTVQVYESTP 997
 Qy 756 TVPLPRLPREPCGHLKTSCEBIRRKPDOWAQHTOKAPLVSS-----TL 797
 Db 998 LVPM-GSVGQVOVS-----QPAVASTQOPTTSSQAOVLESTQVSQAAPPEQT 1046
 Qy 798 PVATOSPTPSPPLFS-----VDFRADFS-----SVSGCKFEEDHLSHVSPWCGTIG 845
 Db 1047 PITOSQOPTQPVPLVTSADSAHSDVAGSMGSDGENAPSSGRHEGRTKHYRK--SVRS 1103
 Qy 846 SCINAIDSERKDVIAN-----SNAVIMDLUSGDVTRVRVHFETQRTKEEPIIPTSDGP 900
 Db 1104 RSRHEKTSRPKURILAVNKGDRRVVCOLQETHNRKRVTFKDLDGDNPEELATIVNND 1163
 Qy 901 IISKWGAISRS-----RTGHTDPVQ-----ATASQ 928
 Db 1164 IL---AIEERSFVAVRETEKABMLEDVSVPREGOCLESLOGKDDYGFPSQKLE 1219
 Qy 929 GSATKPISVSPYVPMVNAVDSRWSSYGENATSSAHYVERDRFIVTDLGHRKHS---TG 985
 Db 1220 GEFKQPIAVSSMPQQGIVPITS-----SLTQVWHSGAR-RFPIVSPVPESLRESKFTS 1271
 Qy 986 DLIS-LELOQAKNSNLQOBANALAMQKNSLDEGR 1022
 Db 1272 DISDPVVAStSQAPGMNLSHASSLSQLQAPSELKHQ 1309

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; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(674)
; OTHER INFORMATION: Ceres Seq. ID no. 1828460
; US-11-096-568A-27756

Query Match 3.3%; Score 203; DB 6; Length 674;
Best Local Similarity 23.1%; Prd. No. 7.2e-05;
Matches 137; Conservative 58; Mismatches 209; Indels 190; Gaps 30;
Locality: (1)..(674)

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Qy 353 HLELANNID-----PYPDAYSPTWBDLE----NAMWA[KTIVWHLVLD]TQNY 396
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Db 355 HKKLLFELDLISNNRFVGKFPPNVLSLPSLKFDLDRYNEFGSIPSKLFDKBIDA[FLHNH 94
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 397 RKKGHETPOQPNISKYKTSMCDDLRQOGGCPRTNCFAHSOEBELEYKURRANKINA--- 452
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 395 RFMFGIPENKNSPVALVIAAD-NDG[GCTPG--SIGLMGKTBELIILNDNUTGLPP 150
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 453 -----TVTRTEPL-LNKVG[VNTVTTAGN]SV---ICSTET[GKV[PSTNG]TSNA 501
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 151 QIGNLKNVTFDISFR--LSCGPLPSSIGNMKNSLEOLANVANRFTGVIPSSICQLSNLEN 208
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 502 SVSQLJSRSTGSTLRALETVKVG-KVGANG-----QNAACPSADSUTENK 546
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 209 ---FTYSSNFTGDA[RCVALIGDNVWVNGSMNCIDGKEODRSSKECSSPASRVDCSK 264
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Qy 547 IGS-----PKTPVSWA-----ATSGAPS 567
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 265 FGCNNFFSPPPPFSKMSPTVRLVLPPEPSSONSPTERATPBPSSKMSPFRATPBPSS 324
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Qy 568 -VGTELNSV---QKS[SPFLTRV]PVYPHSENINQFQDPRQI[PFEPV]PQQTGYYPP 622
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Db 325 KMSPSFRATPBPSSKMSPSVKA[VPPPPPE]YERSPPPPESSEMPSVRAVP---PPP 379
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Qy 623 PTYVAGCVA[PCY]FV[NSV]V[NSV]LPP-----ASMPYADHYSTFSPR 664
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Db 380 PLSPPPPSP-PPPYIYSSPPPPSPSPSPSP-PPPYIYSSPPPVNCPTTOSPPPKYEQTPSPR 438
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Qy 665 D--RMSSPY---OPPRQPY--GPVPIVPSGM[A-----PVYDSRRIRWPMPY 706
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 439 EYPPSPSPPYIYQYTSSPPPYIYATOSPPPPRPTTYAVOSPPPPPVY-----YPPV- 491
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 707 QRDDITRSNLSPMDVMHSSVIVQTSLRERYNLDGYTSVACQ--PPSEPRTTVPLREPC 764
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 492 -----TASPPPPVYVTPVQSPPPPPV--VYSPPVQSPPPPPVYVPPVQSP- 538
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 765 GRUKTSCEEQRRKPDOWAQMTQKAPLVSS-----LRAVATOSPTPPSPLF 811
| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 539 -----PPSPVYY----PPVTQSPPPPPVYLYPV-TQSPPPPSEPVY 573
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Search completed: May 24, 2006, 12:53:32
 Job time : 116 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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 OM protein - protein search, using sw model
 Run on: May 24, 2006, 12:51:45 ; Search time 10 Seconds
 (without alignments)
 1326.457 Million cell updates/sec

SUMMARIES

1	Ltd.
2	seconds
3	nts)
4	cell
5	updates/sec
6	VANGKMNNS 1191
7	140 2.3 1003 6 US-10-953-349-1431
8	28 2.3 139.5 6 US-10-953-349-1430
9	29 2.2 139.5 6 US-10-953-349-8749
10	30 2.2 139.5 7 US-11-289-3849
11	31 2.2 139 6 US-10-953-349-5551
12	32 138.5 2.2 227 6 US-10-953-349-20011
13	33 137.5 2.2 542 6 US-10-953-349-30541
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16	36 137 2.2 564 6 US-10-511-937-2557
17	37 2.2 136 6 US-10-953-349-15256
18	38 136 2.2 173 6 US-10-953-349-1525
19	39 136 2.2 812 7 US-11-293-687-3673
20	40 136 2.2 4373 7 US-11-118-524-2
21	41 135 2.2 293 6 US-10-953-349-31470
22	42 134 2.2 681 6 US-10-953-349-10919
23	43 133.5 2.1 454 7 US-11-293-673-3959
24	44 133 2.1 778 7 US-11-293-673-3043
25	45 132.5 2.1 161 6 US-10-953-349-18169
26	51
27	RESULT 1
28	US-10-480-434A-14
29	; Sequence 14, Application US/10480434A
30	; Publication No. US20060105403A1
31	; GENERAL INFORMATION:
32	; APPLICANT: DALLA VENEZIA, NICOLE
33	; APPLICANT: MAGNARD, CLEMENCE
34	; APPLICANT: SINTILNIKOVA-ERARD, OLGA
35	; TITLE OF INVENTION: BRC1/ACC ALPHA MOLECULAR COMPLEXES, DIAGNOSTIC AND
36	; TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
37	; FILE REFERENCE: 0512-1194
38	; CURRENT APPLICATION NUMBER: US/10/480,434A
39	; CURRENT FILING DATE: 2003-12-12
40	; PRIOR APPLICATION NUMBER: PCT/FR02/02016
41	; PRIOR FILING DATE: 2002-06-12
42	; PRIOR APPLICATION NUMBER: FR 01/07740
43	; PRIOR FILING DATE: 2001-06-13
44	; PRIOR APPLICATION NUMBER: FR 02/02789
45	; PRIOR FILING DATE: 2002-03-05
46	; NUMBER OF SEQ ID NOS: 23
47	; SOFTWARE: PatentIn Ver. 3.2
48	; SEQ ID NO: 14
49	; LENGTH: 1812
50	; TYPE: PRT
51	; ORGANISM: Mus musculus
52	; US-10-480-434A-14
53	Query Match 2.8%; Score 177; DB 6; length 1812;
54	Best Local Similarity 18.2%; Pred. No. 0.036; Gaps 55;
55	Matches 232; Conservative 167; Mismatches 470; Indels 406; Gaps
56	Sequence 13469, A
57	Sequence 13468, A
58	Sequence 13467, A
59	Sequence 16346, A
60	Sequence 799, APP
61	Sequence 4492, AP
62	Sequence 21437, A
63	Sequence 9736, AP
64	Sequence 9735, AP
65	Sequence 9737, AP
66	Sequence 13782, A
67	Sequence 13782, A
68	Sequence 8748, AP
69	Sequence 3340, AP
70	Sequence 312, APP
71	Sequence 23677, A
72	Qy 10 EFLSCPICYNEFDENVHKPISLGCSHTVKCQLNKLHRK---ACPFQDQTAINTIDVL 64
73	Db 20 KILEBCPICL---ELIKEPVSTKCDHIFCKFCMQLNQKKGPSQCPLKRNBIT---- 69
74	Qy 65 PVNFALLQLQVGAQVDPHQSKLNSLNQGENKHVEAKKCVVEDIALYLKPGLSGKGKVASLNQS 124
75	Db 70 --- KRSIQLGSTRSQLA---EEILRIMAFELDTGMQLTNGF 105
76	Qy 125 ALSRPWORKLVTLVNCOLVSEBGRYFAMRAARSLSGERTVTULQHONPOQDSLANSANLWAAV 184
77	Db 106 SFSPKGANN-----SCERLNEEASI----IQSVGYNRVRIPQEP----- 142
78	185 RARGCQFLGPMPMQEALKLVILALEDGSALSRKVLYLFVWYORLEPRPPQASKTSIGHWQ 244
79	Db 143 -----GNTLKDSDL-----GVOLSNLGINVRSKN--RQTQPRKRKV--YIE 180
80	Qy 245 LYIRASCFKTKTRDE---DSSLWOLKEERFSYEALRREHQDQIVHIAAMEAGLR-1SPEQ 299

Db 181 LDDSDSEETVTKPGDCSVRDBELLOPAPOEADEG--KLSAEEACEFSBGRNTEHQ 238
 Qy 300 WSSLLYGDLAHKSHMOSIIDKLQSPSPFAKSQVQELTIVLQRTGDPANLNLRPHIELLAN 359
 Db 239 CSDDANTPENATE-----RHEPK-COSISINCVCPGTAHASSLQPERSLL 289
 Qy 360 IDPNPDAVSPTWEQLINAMVAKTVVHGLUDFFIONYSR---KGHBTPQOPNSKXKTSM 415
 Db 290 IEDRMNA----EKAECFNKSKORGIA--VSQOSRWAASKGTNDRQVPSGEKV- 337
 Qy 416 CRDLIQQGGCPRGTCNTCTFAHSQEBELKYLRANKKINATVTFPLANKVGVTNTVITAGN 475
 Db 338 -----GPN----ADSLSDREW-----THP--OSLCPENSAGTDTVP 368
 Qy 476 VTSVIGSTE-----TTGKIVPSTNGI----SNAENSYSQLISRSSTDPLRAETVK 523
 Db 369 WITLNSVQKVNNEWSRTGEMILTSASARHESNAAVTLEVENEVUDG--GFSSSRK 425
 Qy 524 VGKVG-----ANGONAAGPSADSUTENKIGSPPKTPVNSVAATSAGPSNVTELNS 574
 Db 426 TDLYTDPHPHTIMCKSGGRDFSKPKVEINISDKFGKEYQRKCSR-----PHLNH 473
 Qy 575 VPKQKSPRPLT--RVYPYPPHSENIOFQDPRTQIPFEPVPOZTQGYPPRPTVPG--V 629
 Db 474 VTEIIGTFITEPQTQBPFTKLUKRKRSTSLOPEDFIKKADSAGVQRTPDNINOQTDLM 533
 Qy 630 APCVPFRVRSNWPESSLPPASMPYADHYSPSPROMMSFYQPPPPQVGPVPPVPG 689
 Db 534 EPNEQAVISTTNCENQCIKTAGEN----OKEKAHPTTSIRKE----- 572
 Qy 690 MIAVPVDSRRTRWPPMVQRDDIRSNSLPPMDV--MESSYVQTSLRERYNSLDGYVA 746
 Db 573 -ASTAGAKS1-----SNSVSDLEELVNHFSSAKPKKORLRS----SIR 612
 Qy 747 COPPSRERTTYVLPREPGHLKT----SCBQIRRKEDQDMAQHOTOKAPLVSTLVATO 802
 Db 613 CALPLEPISRNNSP--PTCAELQOIDSCSSEEFKKKNHSNQOPAGHLREPOLIEDTEPADA 671
 Qy 803 SPTPPSPLFSTVDFRASESYESGKTFKEDHFLSHYSPWSCCGTISCNAIDSEPKDVIANS 862
 Db 672 KNEPN-----BHTKR-----RASDAPPEKLMNK 697
 Qy 863 NAVMLMDLSDGVKRRVALFETORTKEEDPIIFPSDGPIISKWGAISRSSRGTGHITDPV 922
 Db 698 AGLTCSSS-----PRISQGPVN-----SPTQGTELETR 729
 Qy 923 QRTAS-----OGSTIKPLTSVSDVYPPVNAVDSRMSSYNEATSSAHYVERDR 969
 Db 730 QMSDSAELGDRVLGGGPSGKTTDRSBESTSVSLVS--DTPYDTONSVSVDAAHV-- 783
 Qy 970 FIVTDUSGRHKNSTGDLSSLRQQAQSNSLILQOREANALAMQKUNSLDGG----RHL 1024
 Db 784 -----RARTSAQCMWOFVISENPKELVHGSN----NAGSGTICKLKPPLRH- 826
 Qy 1025 TANLISKEIELRNGELOSDYTF-----DATDTKDDIEBELS 1062
 Db 827 AUNLSQLQKVEMDSLUDTOYQNTFQVSKROSSFALESKPRSPQKDAAHSVSKELSPKV 886
 Qy 1063 ALJTD-EFDGQSPRIEELDIO----LGISSONDOLLNGMAVENGHPV--QOHQKEP 1112
 Db 887 AKGKQKERQGQE--FEISHVQVAATVGLIPVPCQEQSKLAADTMCDRGCRICLPPSHRS- 943
 Qy 1113 PRKQKGSIQGLEDVILEBOKTIPTVTSFSQPLPVPSITSNASCHPITVSAGNLILKTHM 1172
 Db 944 -----GENG-LSATGKSGISQNSHIFKO----S/S/SPRESSI----- 973
 Qy 1173 SEDKNDFLKPVANGK 1187
 Db 974 --KTDNRKPLTEGR 985

US-11-293-697-3929
 ; Sequence 3929, Application US/11293697
 ; Publication No. US20050105376A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: H1-A0106
 ; CURRENT APPLICATION NUMBER: US/11/293, 697
 ; CURRENT FILING DATE: 2005-12-05
 ; PRIORITY APPLICATION NUMBER: US/10/108, 260
 ; PRIORITY FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 3929
 ; LENGTH: 577
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-293-697-3929
 ; Query Match 2.8%; Score 171; DB 7; Length 577;
 Best Local Similarity 22.0%; Pred. No. 0.016; Gap 20;
 Matches 98; Conservative 50; Mismatches 147; Indels 150; Gap 20;
 Db 451 NATVRTPPLANKVGVNNTVTTAGNVISVIGSTETGKIVPSTNGTNSAENSYSQLIRS 510
 Qy 511 TDSLTALETVKKGKVGANGQNAAGPSAATVRENKIGSPKTPVNSVAATSAGPSNVGT 570
 Db 51 KNTSPLRYHT-----SSTHRREVPTSTMTKFTKTSTGTRTPVAK--TTSASSRRLPT 102
 Qy 571 BL--NSVPOKSSPFLTRPV-----YPPHSENIOFQDPRTQIPFEPVQY---- 613
 Db 103 PFTTHSPPTGSSPFESTGPMWTSFOTTIVTPTPSH-----POTLPTHVPPFSTSLV 155
 Qy 614 -----POTGYPPPTVVA----- 627
 Db 156 TPSTHTVIIHTQMATSSAHSIHTPCTGVPPPTLKATGSTHTAPMTVTTSGTSOTHSS 215
 Qy 628 -GVACPVFRYRNN_VPE--SSLRPA-----MPYADHVSPTSPDRMMNSPYOPPPQ 678
 Db 216 FSTATASSSFISSSMLQNSSSRPPSSPITQMLPLLSATTPVSTNQLSFSFSPPSA 275
 Qy 679 PYGPVPPVPSGMWAPYDSSRRIWRPPMVQRDDIRSNSLPPMDVMISSVWTSLRERYNS 738
 Db 276 PSTVSVSPVSSHSPOTS-----PSVGTTSFSFV--SAP---VHSTTISGSHSLLST 323
 Qy 739 LDGYYSVACQP--PSPF-----RTVPLPBPCEPCGHLKTSCEBQIRRKPDDOMAQHQTQKA 790
 Db 324 HPTTASVSSASLPFPSSPASTIRATLP-----HTISS 356
 Qy 791 PL-VSSTPLVA--TOSPTPPSPLFS 812
 Db 357 PFTISALNLPISVTVTPPSHLAS 381
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 US-10-953-349-9275
 ; Sequence 9275, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; TITLE OF INVENTION: ENCODED THERBY
 ; FILE REFERENCE: 2750-157PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953, 349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 9275
 ; LENGTH: 3429
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana

US-10-953-349-9275

Query Match 2.7%; Score 166.5; DB 6; Length 3429;
 Best Local Similarity 19.2%; Pred. No. 0.33; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

Qy 247 YRASCFKVTKRDBDSSIMQLKEFRSYEARLREHDAOI VHIA MEAGL RISPEQWSLLYQ 306
 Db 1190 YLESILIRESKKEDEAPV- -LDDDALNDLIARRESEIDIFESIDKORKENEMETWNILVHG 1247

Qy 307 DLAKH-SHMOSI1DKQSPSF------AQSVOELTIQORT----- 341
 Db 1248 PGDSFAHIPSIPSLVYTEDDILLYETMKLNDVPMVAKESTVGMRKRDGSMMGLDTHQY 1307

Qy 342 GDPANJNLRPHLELLANID-----PNPDVSPTWOLENAVMAVKTUVHGLDFION 394
 Db 1308 GRGRKRAREVSYEEKUTEEBEKLCOESPSPSQKGEGRSRSLANDTSNIP----VEN 1362

Qy 395 YSRKGHBTPOP-OPNSKYKTSMCRDLRQOGGCPRGNTCTFAHSQELEYKVRLNKKINAT 453
 Db 1363 SS---DTLPLTSPTOAITVOMPEPVRO-----SHTIKEETQIKRGRGPK---- 1406

Qy 454 VTFPLANKVGNNTVTTA-GNVIVSIGSETTGKIVPSTNGISIANSVSQLSRSTD 512
 Db 1407 -RTDKALTPVSLSAVRTQATQNAIS---SATGLDFVSSDKRLEASHPTSSLALTSPD 1462

Qy 513 -----STRAELETVKVKUGANGONAAG--PSADSVTENKIGSPPKT 53
 Db 1463 LSGPPGROSPLASPAPTPIRGRGRGRGRRVEGVHLGSNSITOR----- 1514

Qy 554 PVSNVAATSAGSPNVGTELNSVQKSPFLTRVP-----VYPHHS----- 593
 Db 1515 --TETATSLASDAEATKF- -ALPRSAEIVSVRKVKANBGSTSNDQVSPVHSATTALRD 1570

Qy 594 -----ENYOFPDPRTOIPFEVPOQY----QTYVYPPPTVP----- 626
 Db 1571 KADKDLDAPPFDGSHVQTLVLENNSERKAFAVKKRPLIQGVSSQHPGNQKQPLDP 1630

Qy 627 -----AGVACPVPREVRSNVNPESLPPASMPY-ADHYSTFSPRDR--MNSSYQ-- 673
 Db 1631 VTSSTLGGPVQVNQNAVSSVCDGSKSPSERTVYALQVTTAPSATLMSQSDAT 1690

Qy 674 -PPPPQYGP-----VPPVSGMYAPVDSRRIWRPPMY---QRDDITRSNLPPM 720
 Db 1691 LMSSSQPGVSTVEAQANVPSLPAALPA---KRRVNLPLSGETPKRGRGPQPLPAT 1746

Qy 721 DWHSSVYQTS-----REVMYLDG---YVSACQPPSERRTVLPRECGHHLTSCE 772
 Db 1747 DA--SSARSTGLTPOLEVKVGNLISGTAKAFDVAKEBOPHFSOSVA----PDIHSSGSL 1799

Qy 773 EQIRR-----KPDQMAQYHTQAKLVLSSTPVATQSPTPPSP- 809
 Db 1800 QBRRTSGTCGARKOTADVTDVARMKKEFSETSULKHKGEPASATTRNVDQSPG 1859

Qy 810 --LFSVDFRADFSESYSGTKEE-----DHLSSMSPWCGTGTSCINAISE 854
 Db 1860 EMNLHVTETHK- -AEDSSGLKQEAQALYNLSKADKLVSDIPRVPGDLITSGSVAN--- 1912

Qy 855 PKDVIANSNAV-----IMDLGGDVKRV--HLFEE-----QRTKEE 890
 Db 1913 -KDVDIGSSKAENELVKGDGDVSSVIOISLGNLTAKSLEKCTADOLIGEKLSOE 1971

Qy 891 DPPIPSDGPIKISKWGAISRSRTGHTDVOQATASQSATKPIVSYDVFYNAVDSR 950
 Db 1972 GETTPASDGETCHL- -AEETASSLSYVRSEP--TASASTHEPLTDKLENKISFODE- 2025

Qy 951 WSGNEATSSAHYVERDRFTVTDLSGHKKSISTGDLISLEQAKNSNLQREANALA 1010
 Db 2026 -----VTKLNGDKEAI--LLSE-EQTNVNSKI--ETNSE 2057

Qy 1011 MQOKWNLSDGEHHTLNLSSKELELNGELOSODYTEDATTPDRTDELELSALDDEPD 1070
 Db 2058 LQA--SRTDEVPHVD---GKSVUDVANQTVKED-----BAKHSVEIOSSMLEPDEL 2103

US-10-953-349-9274

Query 1071 GOSEPIEELDQ-IGISQNDQLINGMAYENGHPVQHQKEPPKOKKQSQSLGEDHVILEE 1129
 Publication No. US/10953349
 Best Local Similarity 19.2%; Pred. No. 0.33; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

Qy 1130 QTKLIVTCSQPLPVSIASCRPITSVAGN--LIKTHWSEBDKDFLKVANG 1186
 Db 2148 -----PEESVfvQ---GVGRPKVGTADTQMEDINDAKLUVGCSVESEKEKTLQSLIPG 2198

RESULT 4

US-10-953-349-9274
 Sequence 9274 Application US/10953349
 Publication No. US200610107345A1

Best Local Similarity 19.2%; Pred. No. 0.33; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: ENCODED THERBY
 TITLE REFERENCE: 275-0-1579PNS2
 CURRENT APPLICATION NUMBER: US/10-953, 349
 CURRENT FILING DATE: 2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 9214
 LENGTH: 3438
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana

US-10-953-349-9274

Query Match 2.7%; Score 166.5; DB 6; Length 3429;
 Best Local Similarity 19.2%; Pred. No. 0.33; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53; Matches 219; Conservative 151; Mismatches 439; Indels 331; Gaps 53;

Qy 247 YRASCFKVTKRDBDSSIMQLKEFRSYEARLREHDAOI VHIA MEAGL RISPEQWSLLYQ 306
 Db 1190 YLESILIRESKKEDEAPV- -LDDDALNDLIARRESEIDIFESIDKORKENEMETWNILVHG 1247

Qy 342 GDPANJNLRPHLELLANID-----PNPDVSPTWOLENAVMAVKTUVHGLDFION 394
 Db 1199 YLESILRSKESKEDEAPV- -LDDDALNDLIARRESEIDIFESIDKORKENEMETWNILVHG 1256

Qy 307 DLAKH-SHMOSI1DKQSPSF-----AQSVOELTIQORT----- 341
 Db 1257 PGDSFAHIPSIPSLVYTEDDILLYETMKLNDVPMVAKESTVGMRKRDGSMMGLDTHQY 1316

Qy 342 GDPANJNLRPHLELLANID-----PNPDVSPTWOLENAVMAVKTUVHGLDFION 394
 Db 1317 GRGRKRAREVSYEEKUTEEBEKLCOESPSPSQKGEGRSRSLANDTSNIP----VEN 1371

Qy 395 YSRKGHBTPOP-OPNSKYKTSMCRDLRQOGGCPRGNTCTFAHSQELEYKVRLNKKINAT 453
 Db 1416 -RTDKALTPVSLSAVRTQATQNAIS---SATGLDFVSSDKRLEASHPTSSLALTSPD 1471

Qy 342 GDPANJNLRPHLELLANID-----PNPDVSPTWOLENAVMAVKTUVHGLDFION 394
 Db 1372 SS---DTLPLTSPTOAITVOMPEPVRO-----SHTIKEETQIKRGRGPK---- 1415

Qy 454 VTFPLANKVGNNTVTTA-GNVIVSIGSETTGKIVPSTNGISIANSVSQLSRSTD 512
 Db 1474 LSGPPGROSPLASPAPTPIRGRGRGRGRRVEGVHLGSNSITOR----- 1523

Qy 554 PVSNVAATSAGSPNVGTELNSVQKSPFLTRVP-----VYPHHS----- 593
 Db 1524 --TETATSLASDAEATKF- -ALPRSAEIVSVRKVKANBGSTSNDQVSPVHSATTALRD 1579

Qy 594 -----ENYOFPDPRTOIPFEVPOQY----QTYVYPPPTVP----- 626
 Db 1580 KADKDLDAPPFDGSHVQTLVLENNSERKAFAVKKRPLIQGVSSQHPGNQKQPLDP 1639

Qy 627 -----AGVACPVPREVRSNVNPESLPPASMPY-ADHYSTFSPRDR--MNSSYQ-- 673
 Db 1640 VTSSTLGGPVQVNQNAVSSVCDGSKSPSERTVYALQVTTAPSATLMSQSDAT 1699

Qy 674 -PPPPQYGP-----VPPVSGMYAPVDSRRIWRPPMY---QRDDITRSNLPPM 720
 Db 1700 LMSSSQPGVSTVEAQANVPSLPAALPA---KRRVNLPLSGETPKRGRGPQPLPAT 1755

QY 721 DMMHSVYQTSLL---RERYNSLDG---YVSACOPSPSPRTVPLPREPCGHKTSCE 772
Db 1756 DA---SSARSTGLTPOLEVKVNLSCTIKAKDVAKEQPHEQSVA---PDIHSGSLS 1808
QY 773 EQIRR-----KPDQAQHTQAKPLVSSTLPVATQSPPPSP- 809
Db 1809 QEIIRDTSGTGCSSARKQTADVTDVARMKEIFSETSLKHKVGEFSATTRTNVPAQSPG 1868
QY 810 ---LSSVDFRADFSSSVSGTKFEE-----DHLHYSPMSPCGTGSCINAIDSE 854
Db 1869 EMNLHVTETHK---AEDSSGLKNOEALYNLSKADKLVLSDIPHVPGLDTTSGSVAN---- 1921
QY 855 PKDVJANSNAV---LMDLDSGDYKGRV--HLEET-----QRRTKEE 890
Db 1922 -KDVPIGSKYAAENELVKLPGDVSSVQIQLSGNTLTAKSSLKTAQDOLGLKSOE 1980
QY 891 DPIIPFSDGPILISKNGAISRSSRTGHTPVQATSKPISVSDYVPPYNAVDSR 950
1981 GETTPASDGFETCHL--AEETASSLSVRSBP--TASAATPAUTDPLKLNKSFQDE- 2034
QY 951 WSSYGNREATSSAHYVERDRFTVTDLSGHRKHSSTGDLISLQOAKSNSSLQOREANALA 1010
Db 2035 -----VKTINGDKRAI---LSSB-EQTNVNSKI--BTNSEE 2066
QY 1011 MQQKONSLDGSRHHTNLSKETELRNGELOSDYTEDATPKPDRDIELSALDTDEPD 1070
Db 2067 LQA---SRTDEVPHD---GKSVDAQNTKED-----EAKHSVEIQSSMLSPDELP 2112
QY 1071 GOSEPIEELDIO-LGISSONDQLNGMAYENGHPVQHQKEPPKKQKKSIGEDHVILEE 1129
2113 NAGQKHSISIDLQPLVLTSE--NAMSLDD-----KDYDPIKSADIEQ---- 2156
QY 1130 QKTLILVTSQSPLPVVISNASCLPLITSVSAGN--LILKTHMSEDKNDFLKEVANG 1186
Db 2157 ---PEESVFQ---GVGRPKVGTADTQMEDTNDAKLUVGCSVESEEKEKTLQSLIPG 2207

RESULT 5

US-10-953-349-9273

; Sequence 9273, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9273
; LENGTH: 3478
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-9273

Query Match 2.7%; Score 166.5; DB 6; Length 3478;
Best Local Similarity 19.2%; Pred. No. 0.34;
Matches 219; Conservative 151; Mismatched 439; Index 331; Gaps 53;
Db 1239 YLESLLRESKKEEDAPV---LDDDALNDLIARESEEDIFESIDKQRKENEMETWNLVHG 1296

QY 307 DLAKH-SHMSQSIKLUOSPSE-----AKSVQELTIVLQRT----- 341
Db 1297 PGSDSFHIPSIPSLRVTEDDIKLLYETMKLNDVPMVAKESTVGMGRKGDSMGGDTHQY 1356
QY 342 GDPANUJRLRPHELLANID-----PNPDPVSPTWOLENAMAVKTVVHGLVDIION 394
Db 1357 GRGKRAREVSRVERKLUKEEFKLQCOTESPSSPGKGEGBERSLANDTSNP----VEN 1411
395 YSRKGHETPQP-QPN SKVYKTSNCRDLRQOGGCPRGNTCTFAHSQEELKYRLRNKINAT 453

Db 1412 SS---DTLILPTSPTQATIVQPMEPVRPQ-----SHTLKEETOPIKRGRGRPK--- 1455
QY 454 VRTFPLINKIVGVNNVTITA-GNVISVIGSSTETOKIVSINGNSNAENSQSLTSRSTD 512
Db 1456 -RTDKALTPTVPSLAYSRSRTGTGNAIS--SAATGLDPVSSDKRBAASHPTTSSLLTSP 1511
QY 513 -----STLALEYTVKKGKVGANGQNAAG--PSADSYTENKLGSPPKT 553
Db 1512 LSGPPFQSLRASPAPTPTRGRGRRSRGRGAGRGRVRCVILHGNSNSITQR----- 1563
QY 554 PVSNYATASAGPSNYGTELNSVPOKSSPFLTRVP-----VYPPHS----- 593
Db 1564 ---TETATSLASABATKF-ALPRSASETIVSRVUPGANEGSTSNPQDVSPPHSATTALRD 1619
QY 594 -----ENIQYQDPRQIPEFPVQYP---OTGYVYPPPTWP---- 626
Db 1620 KAADKDLDAPPGFDGSQSHVOTLNVLBNNSERKAFAVKKGRLIQGVSSQHGPKNKOPDLDLP 1679
QY 627 -----AGVAPCVRFRVSNNVPESLPPASMPY-ADHYSFTSPRDR--MNSSPYQ- 673
Db 1680 VSTSSTLIGGSPVQNONAVSSVCDSKSSEGRYTALQVTTASDATLPMSSOPSDAT 1739
QY 674 -PPPPROPYGP-----VPPVPSKMYAPYDSDRRIWRPPM---ORDDIRNSNLSLPPM 720
Db 1740 LPMSOPVPGSVEAQBNVSLPA---KRRVNLPSRGETPKRQKRGCPOLPAT 1795
QY 721 DMMHSVYQTSLL---RERYNSLDG---YVSACOPSPSPRTVPLPREPCGHKTSCE 772
Db 772 DA---SSARSTGLTPOLEVKVNLSCTIKAKDVAKEQPHEQSVA---PDIHSGSLS 1848
QY 1796 DA---SSARSTGLTPOLEVKVNLSCTIKAKDVAKEQPHEQSVA---PDIHSGSLS 1848
Db 810 ---LSSVDFRADFSSSVSGTKFEE-----DHLHYSPMSPCGIGSCINAIDSE 854
QY 1909 EMNLHVTETHK---AEDSSGLKNOEALYNLSKADKLVLSDIPHVPGLDTTSGSVAN---- 1961
Db 855 PKDVJANSNAV---LMDLDSGDYKGRV--HLEET-----QRRTKEE 890
QY 1962 -KDVPIGSKYAAENELVKLPGDVSSVQIQLSGNTLTAKSSLKTAQDOLGLKSOE 2020
Db 2021 GETTPASDGFETCHL--AEETASSLSVRSBP--TASAATPAUTDPLKLNKSFQDE- 2074
QY 951 WSSYGNREATSSAHYVERDRFTVTDLSGHRKHSSTGDLISLQOAKSNSSLQOREANALA 1010
Db 2075 -----VKTINGDKRAI---LSSB-EQTNVNSKI--BTNSEE 2106
QY 1011 MQQKONSLDGSRHHTNLSKETELRNGELOSDYTEDATPKPDRDIELSALDTDEPD 1070
Db 2107 LQA---SRTDEVPHD---GKSVDAQNTKED-----EAKHSVEIQSSMLSPDELP 2152

RESULT 6

US-10-559-415-190

; Sequence 190, Application US/10559415
; Publication No. US20060100132A1
; GENERAL INFORMATION:
; APPLICANT: Astrazeneca AB et al
; TITLE OF INVENTION: Diagnostic Method
; FILE REFERENCE: 101073-1P WO
; CURRENT APPLICATION NUMBER: US/10/559,415

Qy 1071 GOSEPIEELDIO-LGISSONDQLNGMAYENGHPVQHQKEPPKKQKKSIGEDHVILEE 1129
Db 2153 NAGQKHSISIDLQPLVLTSE--NAMSLDD-----KDYDPIKSADIEQ---- 2196
Qy 1130 QKTLILVTSQSPLPVVISNASCLPLITSVSAGN--LILKTHMSEDKNDFLKEVANG 1186
Db 2197 ---PEESVFQ---GVGRPKVGTADTQMEDTNDAKLUVGCSVESEEKEKTLQSLIPG 2247

CURRENT FILING DATE: 2005-12-06
 PRIORITY NUMBER: 0313081.2
 PRIOR FILING DATE: 2003-06-06
 NUMBER OF SEQ ID NOS: 191
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 190
 LENGTH: 1809
 TYPE: PRT
 ORGANISM: Homo sapiens - peptide sequence of amino acids
 US-10-559-415-190
 Query Match 2.6%; Score 159.5; DB 6; Length 1809;
 Best Local Similarity 19.1%; Pred. No. 0.33; Mismatches 429; Index 437; Gaps 66;
 Matches 246; Conservative 174; Mismatches 429; Index 437; Gaps 66;
 Qy 48 KACPFDOTAINTDIDVLPVNFAALLQLOLVGAQVDPHOSTKLNSLNLGENKHYEVAKKCVDLAL 107
 Db 351 KSSTSEKKAAEEMEAL-----RQKD---TVMMDAGRANKEVELRKOCKALCQ 397
 Qy 108 YIKPLISGGKGVASLNOS-----ALSRMQRKVLTNLQVLVREGRTAM---RA 154
 Db 398 EIKEALQEBADYAKCRRDWAQFQERDKVAERDSIRT-----CDNLRE-RDRAVSELAEA 451
 Qy 155 ARSLGE-----RIVTELLQHONPQLSANLMAVRARGCQLGPAMOEALKVL 205
 Db 452 LRSDDTRKOKNDVSRKEL-----KEQMSOLEKARR-----OLMAHSHSDAIDTD 503
 Qy 206 LALE-----DGSALSRKVVLFLVQRL-BPRFQ-----ASKTSIGHVQLLYRASC 251
 Db 504 MEWETEVVEREFERETEDIDKALGFDMAEGVNEPCPGDCG-FVTUDKGSTADGRVND 563
 Db 252 FKVTKRDESSIMQLKEBEFRSYEAL-----RREHDAQIV---HIAAM---EA 291
 Db 564 WILRINDVD-----LINKDKKKQKIKALLNGEATINMVVRKKSIGGKVTPHLNLSQKDS 620
 Qy 292 GIRLSRQW-SSLYGDLAHKSHMOSIDLQKQSPESA-----KSVQELITIVIORTGPANL 347
 Db 621 GISLENGVYAAVLPGSPAEGKSLAVGDRIVANGIALDNKSNBCESSLRSQPSLTL 680
 Qy 348 NLRPHELLANDIDPNDAVSEPTWEQLENAMVAKTVVHGLDFIONYSRKGHETPQPOP 407
 Db 681 SLIK-----VFPQ-----SSSW-----SGQNIFENTKSDDMLSFRAH-GPEVOA 719
 Qy 408 NSK-----YKTSICRDLRQGCGSPRGNTCTFAHSQEELKYLKRNRKINAT 453
 Db 720 HKNRNLJHNINSTQTDIFYDRLDRKEPG-----PPGSSSSFLH----- 759
 Qy 454 VTFPLINKVGNNTVTTAGNIVS1GTSRTRGKIVPSTNGISNAENSYSQLRSTD 513
 Db 760 -KPFP-----GGPLCOPQCPA-----SERSLSSFRSDASD 792
 Qy 514 TIRALETVK-----KVKGKGANGQNAAGPSADSVTENKIGSPPKTPVNVATSA 563
 Db 793 RGGGLDVNRGRPLRPLPTETEGPGCG-----EASLDKADKSEGNSGGWPKAMNSTA----- 846
 Qy 564 GFSNVGTELNSPQKSPFLTRPVVPHSENQYQODPRTQIPFREVPOY-FQGTG----- 618
 Db 847 -----VPEKUS-----VKKPKORKSTF-DPNT-----FKRPQIPPKIDYLLPG 884
 Qy 619 ---YPPPTVPAF-----VAPCVTFREVSNV-----PESSL 648
 Db 885 DQPAHSPQSKRAGPLTPPKPR-----RSDSIKEFHRLTSSSEBATLGSSPSTSPPSALP 942
 Qy 649 P-----ASPYADHSTFSP-----PESSL 666
 Db 943 PDVDPGCPMPHASPPRKARVRIASSYYPPEGEDSSHAPAKSCDDEDLTQSOKYDELQKRR 1002
 Qy 667 MNSSP-YQP-----PPPOPCPVPPVPSGMVAPVDSRRI 700
 Db 1003 PKSAPSPRKPKAQWVPAQFLEQKCPVAPASGELSPQLOEWAP-----YSPGHSSRHS 1054
 Qy 701 WRPMWYQDDITRSNSLUPMDNHSSYQTSLSRERYNSLDGYSYVACQPRSPRPTVPLP 760

Db 1055 -NPPLYPSRP---SVGTVPRSLTPSTVVS\$1RNPIYTVRSHRVGCPSSPAARDAGPQG 1110
 Qy 761 RPBCGHULKSCEBOIRKPD---QMAQKHYQKAPLUSVATQSPSPSPSFVDFR 816
 Db 1111 LMR-----SYHOHQGLSLDLSHRTCSDSYNSRATHGNSLSPSARLUGSS---NLQFK 1160
 Qy 817 AD-----FSESVSGTKFEEDHLSH-----YSPWSGCTGSCINAIDSE---PKD 857
 Db 1161 AERIKPSTPRYPRSVGS- ERGSVSHSECSTPPSPSPNIDTLCSSQSTSASLPR- 1217
 Qy 858 VIANSNAVLMPLDSDGVKRYHFLFETTORTRKEEDP1PF-----SDGPIISKNGAIS 909
 Db 1218 -LAVNPAVL-----GERKDPRYVEEPHRHVQVKGSEPLGJSIVSGEKKGIYVSKVTVGS 1271
 Qy 910 RSSRTGYHTTPV-----QATASQ-----GSATKPKISV-SDVPPWNVAWSRNWSSY 954
 Db 1272 IAHQAGIEYGQOLLEENGJNLSRATESQCARLITLIGOQCDTTLAONPRPHOLSS----- 1326
 Qy 955 GNEATSAHYVERDRFTVTDLSGHR---KHSSTGDLISLLELOQ-----AKENSLLQREA 1006
 Db 1327 --HSRSSSHLDPAGHTSITLQSGSTTPHEPSVSDPL-MEQDEGPSPTPPAKQSSRRIAGDA 1383
 Qy 1007 NALAMQO-----KWNSLDEGHHTLUMLSKIELRNGELDSYTERATDTKPR----- 1055
 Db 1384 NKTTLEPVRVFTKSOLELGHLC-----GGNLHGUVFAEVEDDSPAKGPDGLV 1432
 Qy 1056 --DIEBLSALDTDEPDQSQSPIEI 1079
 Db 1433 PGDLIBYGSLDV-----RNKIVVEE 1453
 RESULT 7
 US-10-559-415-2
 ; Sequence 2, Application US/10559415
 ; Publication No. US20060100132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Astradenea AB et al
 ; TITLE OF INVENTION: Diagnostic Method
 ; FILE REFERENCE: 101073-1P WO
 ; CURRENT APPLICATION NUMBER: US/10/559,415
 ; CURRENT FILING DATE: 2005-12-06
 ; PRIORITY APPLICATION NUMBER: 0313081.2
 ; PRIORITY FILING DATE: 2003-06-06
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 1919
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ;
 US-10-559-415-2
 Query Match 2.6%; Score 159.5; DB 6; Length 1919;
 Best Local Similarity 19.1%; Pred. No. 0.36; Mismatches 429; Index 437; Gaps 66;
 Matches 246; Conservative 174; Mismatches 429; Index 437; Gaps 66;
 Qy 48 KACPFDOTAINTDIDVLPVNFAALLQLOLVGAQVDPHOSTKLNSLNLGENKHYEVAKKCVDLAL 107
 Db 461 KSSTSEKKAAEEMEAL-----RQKD---TVMMDAGRANKEVELRKOCKALCQ 507
 Qy 108 YIKPLISGGKGVASLNOS-----ALSRMQRKVLTNLQVLVREGRTAM---RA 154
 Db 508 EIKEALQEBADYAKCRRDWAQFQERDKVAERDSIRT-----CDNLRE-RDRAVSELAEA 561
 Qy 155 ARSLGE-----RIVTELLQHONPQLSANLMAVRARGCQLGPAMOEALKVL 205
 Db 562 LRSDDTRKOKNDVSRKEL-----KEQMSOLEKARR-----OLMAHSHSDAIDTD 613
 Qy 206 LALE-----DGSALSRKVVLFLVQRL-BPRFQ-----ASKTSIGHVQLLYRASC 251
 Db 614 MEWETEVVEREFERETEDIDKALGFDMAEGVNEPCPGDCG-FVTUDKGSTADGRVND 673
 Qy 252 FKVTKRDESSIMQLKEBEFRSYEAL-----RREHDAQIV---HIAAM---EA 291

Db 674 WLRLINDVD---LINKDKKQAIKALLNGEAGAINMVRRIKSLGGKVTPHLINLSGQKDS 730
 Qy 292 GLRIPPEQW-SSLVYGLAHKSHMQSIIIDKQSPESFA--KSVQBLTVIQLTCDPANL 347
 Db 731 GISLENGVYAAVALPCSPAAGSLAVGDRIVANGIALDNKSLNCELSLRSCDSLTL 790
 Qy 348 NLRPHLELLANIDPNPDAVSPTWEOLENAMAVKTVVHGLDF-QNSRKGHETPQPOP 407
 :
 791 SLK----VFO----SSW----SGNIFENIKSDKMLSFRAH-GPEVOA 829
 Qy 408 NSK-----YKTSMCRDILRQQGCGCPRTGNTCAHQSBELEYKLRLNNKINAT 453
 :
 Db 830 HNKRMUJQHNNTQDIFYDLERDKEPG--PPGSSSEFLH-----
 Qy 454 VRTFPLINKYGVNNFTVTAGNIVSIVGSTETTGKLVPUSTNGISNAENSYQLSRSSTD 513
 :
 Db 870 -KPFP-----GGPLQCPOACPSA---SERLSSFRSDASGD 902
 Qy 514 TRLALETVK-----KVGKVANGQMAAGPSADSVENTKIGSPPKPVPSVNAATSA 563
 :
 Db 903 RFFGLVTDVRGRPLLPRTETEVCPGCVG--BASLDKADSEGSNSGGTWPKAMLSSTA--- 956
 Qy 564 GFPNVGTELNSVPQKSPFLTRVPUVPHSENIOYQDPRTOQIPPEVPOY-PQTGY--- 618
 :
 Db 957 -----VPEKUS-----VKKPKKORKSIF-DPNT--FRKRQTPPKIYLLPG 994
 :
 Qy 619 ---YPRPPPTVFG--VAPCVPVFVRSNNV-----PESSL 648
 :
 Db 995 PGPAHISPOPSKCKRAGPLTPPKER--RSDSIKKQRLETSSSEATLVGSSPSTSPPSALP 1052
 :
 Qy 649 P-----ASMPYADHYSITSP-----RDR 666
 :
 1053 PDVDPGEPBPMHASPPRKARVTRASSYYPEGDGGDBSHLPAKKSDEDLTSQVTDLGOKRR 1112
 Qy 667 MNSSP-YQP-----PPQPGFVPPVSGMYAPVUDSRRI 700
 :
 Db 1113 PKSAPSFRPKLAPWVIAQFLEOKVCPASGLSPSPELQEWAP-----YSPGHSSRHS 1164
 Qy 701 WRPWMYQRDDITRSNLSLPPMDVMHSSYQTSLSRLERYNLSLDGYSVACQPPSEPRTVPLP 760
 :
 Db 1165 -NPPLYPSR-----SVGTVPRLSTPSTVSSILRNPIYTVRSHRVGFCSSPPARDAGPQ 1220
 Qy 761 REPGCGHLKTSSEBQIRKPD---QHAYQHOTKAPLVSSTUPVATQSPTPSPSPSVDER 816
 1221 LHP-----SVHQGRILSDLSDLSHRTCSDYSEMRAHTGSNSLLESSARLGSSS---NLQFK 1270
 Qy 817 AD-----FSESESGTKFEEHDUSH-----YSPWSCCTIGSCINADE--PKD 857
 :
 Db 1271 AERIKUPSTPRYPRSYGS-----ERGSVSHSECSSTPPQSPLNIDTLLSSCSQSTSASTLPR- 1327
 Qy 858 VIANSNAVLMDLSDGVKRRVHFETORRTKEBD1PF-----SDGPIISKWGAIS 909
 :
 Db 1328 -IAVNPSRL---GERRKDRPYVERPRHVVKQKGSEBPLGISIVSCEKGIGYVSKTVGS 1381
 Qy 910 RSRTGHTTTPV-----OATASO-----GSTAKPFSV-SDVYPPVYNAVDWSNWSSY 954
 1382 IAHQAGLEYGDOLLEFNGINIRLRSATEQARLITIGQODTITILAQYNPHQISS--- 1436
 Qy 955 GNEATSSAHYVERDRFVTDLSGHR - KHSSTGDLISLELOQ-----AKNSLIIQREA 1006
 :
 Db 1437 --HSSRSSHLDPGTHSTLOGSGTTPEHPSVIDPL-MEQBGPSTPAKOSSSRAGDA 1493
 Qy 1007 NALAMOO-----KWNSDGEGRHLTNLISKEIELNRNGELOSITYTEDATDTKDR----- 1055
 :
 1494 NKKTLEBRVVFJKSQUELGVL-----GGNLHGFWAEDDSSPAKGFDGLV 1542
 Qy 1056 --DIEBELSALUTDEPPGQSEEIEI 1079
 :
 Db 1543 PCDLILBYGSLD-----RNKTVVEV 1563

Sequence 3230, Application US/11293697 ;
 Publication No. US20060105376A1 ;
 GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: HI-A0106
 CURRENT APPLICATION NUMBER: US/11/293,697
 CURRENT FILING DATE: 2005-12-05
 PRIOR APPLICATION NUMBER: US/10/108,260
 PRIOR FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 5458
 SOFTWARE: PatentIn Ver. 2.1
 SEO ID NO: 3730
 LENGTH: 1057
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-293-697-3230

Query Match 2.6%; Score 159; DB 7; length 1057;
 Best Local Similarity 19.6%; Pred. No. 0.17; Gaps 36;
 Matches 146; Conservative 100; Mismatches 264; Indels 234;

Db 554 PVSNVATSA-----GPSNVGETLNS-----V 575
 :
 Db 3 PLRSVIASTSAKNNDLNRNSQGKDCHLHRHFDVPLNQLQRPPQETGERANKYKEEHRRI 62
 Qy 576 POKS--SPFLTRVPPVPHSENIOYF---QDPRTOI-----PFEVP 611
 :
 Db 63 LOBESIDVAFFTIKIGKLEGERENYSRVASSSSSPKSHI IKODMDVERSVDLYKMGHSV 122
 Qy 612 O-YPOTGYYPRPPPTVAGVABCUPRFVRSNVPESSLPPASMP-----YADHYSITSP 663
 :
 Db 123 QSLPQSNFT-----TLSNVVNB--PKPSYPSKEVSNIYGDKOSNALA 164
 Qy 664 RDRMN-----SSPYQPPP--POPYGPPVPPVSGMAY-----VYDSRR1WRPPM 705
 :
 Db 165 AAAANPQTLTSRITSLSKPPPLIKHOPSEVKGIP--HLPHOTASHVTFRNDCSRPT 222
 Qy 706 YORDDTIRNSLPPMDVMH-SVYQTSLSRLERYNLSLDGYSVACQPS----- 751
 :
 Db 223 HL-TVSSINTLRSMPALHRAFPFHPIHSLEREGGSY-SLSPTLTTPVPMVNAGGV 279
 Qy 752 ---ERRTTIVLPRBCRGHLKTSCEQRIRRQDW-----AOYHTOK-----AP 791
 :
 Db 280 QBSQKPLTIPPKDQSQAQNFSSESSL--TEMWRPNNLSEKTEWHEVKSSGKQAA 336
 Qy 792 LVSTTIPVATQSPTPSPLFSDVFRADFSSESVGTCIKEEDILSHYSPWSCCTIGSCINA 851
 :
 Db 337 MASVIVRPPSSSTKTDSPMAPOLASKDRVRSAGAHTKDCIKLAEGETRI--TLPNV 394
 Qy 852 DSEPKOVVIANSNAVLMDLSDGVKRAV-HLFETORTKEEDIPIIFPSDGPIISKWGAIS 910
 :
 Db 395 NSD--SYTHKSEBNFQAVSQSSVPSSVMSAINTMCNTK-TVITSADATSVSSNCG-- 448
 Qy 911 SSRTGHTTDPVATQASGATSKPI-----VSDDYPPVYNAVDWSRNSYMEATS 960
 :
 Db 449 SEVTSSILNTIATSBSCVSSKSVSOPVAQKOECKRUSTTAPVTLAS---SKTGSVWQP 504
 Qy 961 SAHYVERDRFVTDLSGHRKHSSTGGLLSSLQQAQNSNLLQOREANALAMQOKWNSLDE 1020
 :
 Db 505 SGSGF-----TDFTHLKGKA-----ALAAAQYKSN-ASETEPNATKQNLTLASPL 553
 Qy 1021 GRHLTNLISKEIELNRNGELOSITYTEDATDTKDRDIELELSA-----DTBPPGQ 1072
 :
 Db 554 DSTVICSTINKANSVENGQA-----SOTSPQNYHTKLUKAWLTHRSIEEDKNTKMS 606
 Qy 1073 SERPIETL-----DIOLGTSQ-----NDQJLN-----GMA 1098
 :
 Db 607 GNSVSEIKPCSVNLIASTSSDIQNSVDSKLTIVDKVVKDDKVRKAKRTYESGSGDS 666
 Qy 1099 VENGHPVQOHQKOPKPK--QKQOS 1119
 :
 Db 667 DESESKEQRTKROPKPTYKKQ 690

RESULT 9
US-10-953-349-13469
; Sequence 13469, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953, 349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO: 13469
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-13469

Query Match 2.6%; Score 158.5; DB 6; Length 443;
Best Local Similarity 21.5%; Pred. No. 0.054; Mismatches 154; Indels 183; Gaps 22;
Matches 104; Conservative 42; MisMatche 154; Index 183; Gaps 22;

Qy 434 AHSQEELKEYRLRNKKINATVRTPLINKGVVNNTVTAGNVISVGSTETTGKIVPST 493
Db 67 AETQEKLAQKLAQKESSS-----SS 87

Qy 494 NGISNAENSYSQLISRSTDSTLRALETVKKVGKGANGQ-----NAAGPSA 539
Db 88 HSQSNEERSPTDPKKIDNA-----SDANNQQLALALPHQIAQPQAPASA 135

Qy 540 DSVTENKIGSP-----PKPVNSVAAATSGPSN---VGTELNNSVQOKESFFLTRPVY 589
Db 195 PSPPVQOFQSHYQOQQO---QOPPQQQQQMSQQVQPSQPPMQSQVRPSSNVPPYQPN 252

Qy 136 QKASAVTQAFQPPYVIFPPMPN-SALRHPHQYQYLPSDQQRQYRTPQLAQRPQPSQT 194

Qy 590 P-PHSENIVQFQDPRTQIPFVFVQFQRTGY-----YPP-----PTVPGAVACVPR 635
Db 203 PSPPVQOFQSHYQOQQO---QOPPQQQQQMSQQVQPSQPPMQSQVRPSSNVPPYQPN 260

Qy 636 FVRSNNVPPESSLPPASMPYADHYSTRSPR--DRMNSPY-----QPPPROPYGP 682
Db 261 --QATNPSPAETLPNSWAMQMOPYSGVPPQGSNRADAIPIYGAGRTVPPQPPQOMKSS 318

Qy 683 VPPVPSGMAYAVDSRIWRPPMQRDDIIRSNSLPPMDVHSSVYQTSLRERYNSLDY 742
Db 319 FPAPRGEMYGP-----TGSILPALPPSSA-----YMMYDGE 349

Qy 743 YSVACOPPSEER-----TIVPLPREPCGHLKTSCEBTRRKPD--QWAOYHTOKAPL 792
Db 350 GGRSHRPQPHFAQCGYPPVSASLQNPPQSH-----NLWVRNPQSOVTRNHPYNELI 403

Qy 793 VSSTLPVATOSPTPPSPFLSFYDRAFTSEASYSGTKFEE-----DLHSHYSP-- 838

Qy 636 FVRSNNVPPESSLPPASMPYADHYSTRSPR--DRMNSPY-----QPPPROPYGP 682
Db 253 --QATNPSPAETLPNSWAMQMOPYSGVPPQGSNRADAIPIYGAGRTVPPQPPQOMKSS 310

Qy 683 VPPVPSGMAYAVDSRIWRPPMQRDDIIRSNSLPPMDVHSSVYQTSLRERYNSLDY 742
Db 311 FPAPRGEMYGP-----TGSILPALPPSSA-----YMMYDGE 341

Qy 743 YSVACOPPSEER-----TIVPLPREPCGHLKTSCEBTRRKPD--QWAOYHTOKAPL 792
Db 342 GGRSHRPQPHFAQCGYPPVSASLQNPPQSH-----NLWVRNPQSOVTRNHPYNELI 395

Qy 793 VSSTLPVATOSPTPPSPFLSFYDRAFTSEASYSGTKFEE-----DLHSHYSP-- 838
Db 396 --EKLVSMGFRGDHVAVSI-QRMEESQAVDFNSVLDRLLSSVGPQORG 439

Qy 839 -WS 840
Db 440 GWS 442

RESULT 10
US-10-953-349-13468
; Sequence 13468, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953, 349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO: 13467
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-13467

Query Match 2.6%; Score 158.5; DB 6; Length 456;
Best Local Similarity 21.5%; Pred. No. 0.057; Mismatches 154; Indels 183; Gaps 22;
Matches 104; Conservative 42; MisMatche 154; Index 183; Gaps 22;

Qy 434 AHSQEELKEYRLRNKKINATVRTPLINKGVVNNTVTAGNVISVGSTETTGKIVPST 493

Db 740 RYKELECOOLQFESSAREAMERAILQGEREERAERAILQKEOKAVDQ-----LOKELUVALET 792
 Qy 1038 GELQSDVTEADM----TDKPDDE---JELSAUDTEPD-----GOSPIEE--- 1078
 Db 793 G-IQERDKEARALEETEKLEQERQLESRSBVEERLAGQCLRSKAELSIAKR 851
 Qy 1079 ----TIDIQIG-TSSONDOLINGMAVENGHFVQOHQKEPPK 1114
 Db 852 KERLAILDSQHQIQAQAVOSSERLARDKNASSQLILOKEKEK 893

RESULT 14
 US-11-293-697-492
 ; Sequence 4492, Application US/11293697
 ; Publication No. US20060105376A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT APPLICATION NUMBER: US/11/293, 697
 ; CURRENT FILING DATE: 2005-12-05
 ; PRIOR APPLICATION NUMBER: US/10/108, 260
 ; NUMBER OF SEQ ID NOS: 3458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4492
 ; LENGTH: 950
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-293-697-492

Query Match 2.4%; Score 152; DB 7; Length 950;
 Best Local Similarity 19.9%; Pred. No. 0.35; Mismatches 337; Indels 266; Gaps 44;
 Matches 178; Conservative 114; Mismatches 337; Indels 266; Gaps 44;

Qy 42 LNIKLHKACPF-----QPAINTIDNUVNFAILQVQAVPQHQSIKLSNLGE--- 91
 Db 109 VNKLRQEALDLELQMKOKQPIAGKQKEIKQLOIAIDSL-DSKDPKSHMKQSGKEQ 167
 Qy 92 ---NKHYE-----VAKKCVEDALYLKPLSLGGKGKVASINQSAISRPMO--- 131
 Db 169 LDIMNIKQYQLESRLBLSRILAKE-TEEIKDQLEQTLGQILAN--EALKDQEVLIS 223
 Qy 132 --RKLYTVLNGCOLVVEGRVRAARSLGTRVTLQDOPNQPSANLWAATRARGC 189
 Db 224 GLQEYLGTTIKSQTAQNECRKDERETKLQLRTE--EQBRDQELEI----- 269

Qy 190 QFLGPMEQEEAKLVALLEGSLARKVLUVWQBLERPFPOQTSKTSQHVVOLYRA 249
 Db 270 ---VANDAENMRKELAEL--SALQEO-----HEVNASLQQTQGDLAYEAELEARL 316
 Qy 250 SCKVKTRKDERSSLMWOLKEETRSYEAELL-----EHDAQIVHIAE-EAGURISPE 298
 Db 317 NL-----RDABANQKEELEKVTUQESALQAEERERQAIKNAKQKQSEEKE 369
 Qy 299 QWSLLYQGDLAH-----KSHMQSIIKQSPRFQAKSVQELTIVQ-RTG 342
 Db 370 QENSELHAKLKHLDQDDNNLKLQQLDOPNHLNHWVQGLVRVPEEVAAVDELLRKQKUGTG 429

Qy 343 D-----NRLRHHEELJANIDNPDAVSPTMQLENUM-VAVKTIVHGLD 390
 Db 430 ENNHSPSDVQKSLADLOKQFSELLARSKVERDAQVRKQLEEMALQOEKLTQGQEE 489
 Qy 391 FITQ-----NYSRKGHTP-----OPQPNISKYT 413
 Db 490 FRQACRALEARMENFKQRHARIQOMENETHYLQNLKSMEEIQLSTDQLOADEEKE 549
 Qy 414 SMCDRLRQGGCPRGNTCTFASQEE---LERYRLENKKTMTAVTRTPPLANKGVNNTV 470
 Db 550 RILAQOLE-----LEKKKKLEDAKSQEQVFGQFLDKELKKKKAVATSDKQATABLTIADQKL 606
 Qy 471 TTAGTIVS-----IGSTT-TGKVUPSTNGISVAENSY--QIISRSDSTALET 520

RESULT 15
 US-10-953-349-21437
 ; Sequence 21437, Application US/10953349
 ; Publication No. US2006107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953, 349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 21437
 ; LENGTH: 343
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; US-10-953-349-21437

Query Match 2.4%; Score 151; DB 6; Length 343;
 Best Local Similarity 23.6%; Pred. No. 0.099; Mismatches 131; Indels 118; Gaps 19;
 Matches 87; Conservative 32; Mismatches 131; Indels 118; Gaps 19;

Qy 535 AGPSADSUTENKIGSP-----PKTPVSNVATAGPSN--VGTELNSVQOKSSPPLT 584
 Db 31 AAPSQAAASAVTQAOPOQQPVYIPIPMPN-SALPHQHPOQYOLPLSDQQYRTPOLVAPQPT 89
 Qy 585 RVPVYP-PHSENIQYFQDPRQPRQIPFVPPQYQFQTY-----YPPP-----PTVPGVA 630
 Db 90 PSQVTEPSPPVQFHSYQOPQO-QOPPOOOQQQOQSOQVQPSQOPPMQSOVRPSPNVYP 147
 Qy 631 PCVPRFVRNNVPESSLPPASMPYADHYSTSPTSPR---DRMNNSPY-----OPPP 677
 Db 148 PYQPNT-QATNPSPAEPLPNSMAMQMPYSVQPPQSNRAlipyGGAGRTVQOPPPQ 205
 Db 90 PSQVTEPSPPVQFHSYQOPQO-QOPPOOOQQQOQSOQVQPSQOPPMQSOVRPSPNVYP 147
 Qy 678 OPGYGVPPVPSGMAYAVVYDSRIWRPPMQRDDITRSNLSLPMDVHSVYQTSLRERYN 737
 Db 206 QMKSSFPAPPGEWGB-----TGSIPALPPSSA-----YM 236
 Qy 738 SLGIVSVACOPPSEER-----TIVPUPREPCHLKTSCEEQIRRKPD--QWQYHT 787
 Db 237 MYDGEGGRSHHPQPRHQAQPGYPPTSASLONPQCH-----NLWVNRNPQSOVRNHP 290
 Qy 788 OKAPLVSTLPUVATOSPTPPSPLFSVDRADPSESYSGKTFEE-----DHLSHY 836
 Db 291 YNELI-----EKLVSMGFRGDHVAVSI-QRMEEQGAVDENSVLDRLSV 334
 Qy 837 SP----WS 840
 Db 335 GPQRGGWS 342

Wed May 31 11:47:35 2006

us-10-619-992-2.rapbn

Page 10

Search completed: May 24, 2006, 12:53:48
Job time : 15 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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Title: US-10-619-992-2
Perfect score: 6215
Run on: May 24, 2006, 12:48:59 ; Search time 299 Seconds
Sequence: (without alignments)
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

6082.290 Million cell updates/sec

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6215	100.0	1191	31 US-10-170-205E-31443	Sequence 31443, A Sequence 2, AppI
2	6215	100.0	1191	36 US-10-619-992-2	Sequence 22109, A
3	6215	100.0	1191	49 US-60-452-680-22109	Sequence 13599, A
4	6215	100.0	1191	49 US-60-453-050-13599	Sequence 13599, A
5	6215	100.0	1191	49 US-60-453-135-13599	Sequence 13599, A
6	6215	100.0	1191	49 US-60-466-412-13599	Sequence 13599, A
7	6207	99.9	1191	36 US-10-619-992-4	Sequence 4, AppI
8	5880	94.6	1137	47 US-60-466-73-16	Sequence 16, AppI
9	5880	88.9	1062	31 US-10-170-205E-29971	Sequence 29971, A
10	5525	88.9	1062	49 US-60-452-680-22108	Sequence 22108, A
11	5525	88.9	1062	49 US-60-453-050-13598	Sequence 13598, A
12	5525	88.9	1062	49 US-60-453-135-13598	Sequence 13598, A
13	5525	88.9	1062	49 US-60-466-412-13599	Sequence 13598, A
14	5483	88.2	1048	34 US-10-258-898A-3500	Sequence 8, AppI
15	4416	71.1	869	24 US-09-488-725A-3499	Sequence 3499, A
16	4416	71.1	869	32 US-10-258-898A-3499	Sequence 3499, A
17	4416	71.1	869	32 US-10-258-898A-3499	Sequence 3499, A
18	4066.5	65.4	812	24 US-09-488-725A-3500	Sequence 3500, AP
19	4066.5	65.4	812	32 US-10-258-898A-3500	Sequence 3500, AP
20	4066.5	65.4	812	32 US-10-258-898A-3500	Sequence 3500, AP
21	2685	43.3	1134	51 US-60-675-841-40	Sequence 40, AppI
22	2685	43.2	1134	52 US-60-710-726-114	Sequence 114, AppI
23	2681.1	43.1	1133	52 US-60-731-162-682	Sequence 12, AppI
24	2681.1	43.1	1125	1 PCT-US02-38445-47	Sequence 47, AppI
25	2665.5	42.9	1132	31 US-10-170-205E-7090	Sequence 7090, AP
25	2665	42.9	1132	31 US-10-170-205E-7090	Sequence 7090, AP
25	2665	42.9	1132	31 US-10-170-205E-7090	Sequence 7090, AP
25	2665	42.9	1132	49 US-60-452-680-20520	Sequence 20520, A
27	2665	42.9	1132	49 US-60-452-680-20520	Sequence 20520, A
27	2665	42.9	1132	49 US-60-452-680-20520	Sequence 20520, A
27	2665	42.9	1132	49 US-60-452-680-20520	Sequence 20520, A
28	2106	33.9	421	1 PCT-US00-31653-280	Sequence 280, AppI
29	1712.5	27.6	628	47 US-60-243-734-15	Sequence 15, AppI
30	1712.5	27.6	628	47 US-60-262-905-6	Sequence 6, AppI
31	1593	25.6	306	24 US-09-488-725A-7071	Sequence 7071, AP
32	1593	25.6	306	24 US-09-488-725A-7071	Sequence 7071, AP
32	1593	25.6	306	24 US-09-488-725A-7071	Sequence 7071, AP
33	1593	25.6	306	32 US-10-258-898A-7071	Sequence 7071, AP
33	1593	25.6	306	32 US-10-258-898A-7071	Sequence 7071, AP
34	1593	25.6	306	32 US-10-258-898A-7072	Sequence 7072, AP
35	1593	25.6	306	32 US-10-258-898A-7072	Sequence 7072, AP
35	1593	25.6	306	32 US-10-258-898A-7072	Sequence 7072, AP
36	1593	25.6	306	32 US-10-286-897-7072	Sequence 7072, AP
37	1538	24.7	739	46 US-60-167-217-9685	Sequence 9685', AP
38	1538	24.7	819	26 US-09-614-150A-24915	Sequence 24915, A
39	1538	24.7	819	26 US-09-614-150A-24915	Sequence 24915, A
40	1538	24.7	819	40 US-11-097-143-24915	Sequence 24915, A
41	1538	24.7	819	46 US-11-097-143-24915	Sequence 24915, A
42	1538	24.7	819	46 US-60-191-637-55016	Sequence 25016, A
43	1538	24.7	819	46 US-60-191-681-19706	Sequence 19706, A
44	1492.5	24.5	296	1 PCT-US00-30653-281	Sequence 281, App
45	1492.5	24.5	296	1 PCT-US00-30653-281	Sequence 281, App
14.3	14.3	14.3	195	27 US-09-758-461-704	Sequence 704, App

ALIGNMENTS

RESULT 1
US-10-170-205E-31443
; Sequence 31443, Application US-10-20705B
; GENERAL INFORMATION:

; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: C1001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-170-205E-31443

Query Match 100 0%; Score 6215; DB 31; Length 1191;
Best Local Similarity 100 0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVOAAWTERLSCPICYNEFDENVHKPISLGCSHVKCLNKLUHRKACPFQDQTAINTD 60
1 MPVOAAWTERLSCPICYNEFDENVHKPISLGCSHVKCLNKLUHRKACPFQDQTAINTD 60

QY 61 IDVLVPNFAALLQVLGAQVPDHQSIKUSLNGLGENKHVEAKKCVEDIALYKPLSLGGKGVAS 120
61 IDVLVPNFAALLQVLGAQVPDHQSIKUSLNGLGENKHVEAKKCVEDIALYKPLSLGGKGVAS 120

QY 121 LNQASLRPMQRGKLVLTNLNCOLVVEBGRVRAMAARSLSRGLERTVTELLOHONPOOLSANL 180
121 LNQASLRPMQRGKLVLTNLNCOLVVEBGRVRAMAARSLSRGLERTVTELLOHONPOOLSANL 180

QY 181 WAAVRARGCQFLGPMQEAALKLVLAEDSALSRSKVLVFLVQBLERPPRQASKTSG 240
181 WAAVRARGCQFLGPMQEAALKLVLAEDSALSRSKVLVFLVQBLERPPRQASKTSG 240

QY 241 HVQLIYRASCFKVTKRDEDSLMLQKEFSSYEALRREHDQIYHIAAMEAGLRSPEQW 300
241 HVQLIYRASCFKVTKRDEDSLMLQKEFSSYEALRREHDQIYHIAAMEAGLRSPEQW 300

QY 301 SSILYGDLAHKSHMOSIDKLQSPESPAKSVOBLTIVLORTGPANLNRPHLELLANI 360
301 SSILYGDLAHKSHMOSIDKLQSPESPAKSVOBLTIVLORTGPANLNRPHLELLANI 360

Db 361 DPNPDAVSPTWOLENAMVAKTIVHGLDFQNSRKGHETOPOPNSKTTSMCRDLR 420
361 DPNPDAVSPTWOLENAMVAKTIVHGLDFQNSRKGHETOPOPNSKTTSMCRDLR 420

QY 421 QGGCCPGRGTCTFAHSOEBLEKYLRLANKKINATVRPLANKGVNNTVTAGNIVI 480
421 QGGCCPGRGTCTFAHSOEBLEKYLRLANKKINATVRPLANKGVNNTVTAGNIVI 480

Db 481 GSTETGCKIVPSTNGISNAENSVSOLTSRSTSRTSLRALLETVKVGKANGQNAACPSAD 540
481 GSTETGCKIVPSTNGISNAENSVSOLTSRSTSRTSLRALLETVKVGKANGQNAACPSAD 540

QY 541 SVTENKIGSPPTCPVSNVAATSSAGPSNGTENSVPQKSSLTRPVYPHPSENQFO 600
541 SVTENKIGSPPTCPVSNVAATSSAGPSNGTENSVPQKSSLTRPVYPHPSENQFO 600

Db 601 DPTQTPEEVPOYPOIGYPPPTVPGAVAPCPVPRFRSNNPRESSIPASPYDHYST 660
601 DPTQTPEEVPOYPOIGYPPPTVPGAVAPCPVPRFRSNNPRESSIPASPYDHYST 660

QY 601 DPTQTPEEVPOYPOIGYPPPTVPGAVAPCPVPRFRSNNPRESSIPASPYDHYST 660
601 DPTQTPEEVPOYPOIGYPPPTVPGAVAPCPVPRFRSNNPRESSIPASPYDHYST 660

Db 661 FSPDRDRNNSPQPQPPRQPOGYGVPPVPSRGMVYLPVPSRRTRPPWMQDDITRNSLPPM 720
661 FSPDRDRNNSPQPQPPRQPOGYGVPPVPSRGMVYLPVPSRRTRPPWMQDDITRNSLPPM 720

QY 721 DMHSSYOTSLRERYNSLDGYSVACOPPSPRTPLPBPGIHLKTSEBEIRKPD 780
721 DMHSSYOTSLRERYNSLDGYSVACOPPSPRTPLPBPGIHLKTSEBEIRKPD 780

Db 781 QWAQHMQKAPIVSSTPVATOSPTPSPLSFVDFRADSSESVSGTKFEEEDHLSHYPWS 840
781 QWAQHMQKAPIVSSTPVATOSPTPSPLSFVDFRADSSESVSGTKFEEEDHLSHYPWS 840

Db 781 QWAQHMQKAPIVSSTPVATOSPTPSPLSFVDFRADSSESVSGTKFEEEDHLSHYPWS 840

RESULT 2
US-10-619-992-2
; Sequence 2, Application US/10619992
; GENERAL INFORMATION:
; APPLICANT: Hefenreider, Steven
; APPLICANT: Merklin, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at
; FILE REFERENCE: 00-617-
; CURRENT APPLICATION NUMBER: US/10/619, 992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921, 099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-619-992-2

Query Match 100 0%; Score 6215; DB 36; Length 1191;
Best Local Similarity 100 0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVOAAWTERLSCPICYNEFDENVHKPISLGCSHVKCLNKLUHRKACPFQDQTAINTD 60
1 MPVOAAWTERLSCPICYNEFDENVHKPISLGCSHVKCLNKLUHRKACPFQDQTAINTD 60

QY 61 IDVLVPNFAALLQVLGAQVPDHQSIKUSLNGLGENKHVEAKKCVEDIALYKPLSLGGKGVAS 120
61 IDVLVPNFAALLQVLGAQVPDHQSIKUSLNGLGENKHVEAKKCVEDIALYKPLSLGGKGVAS 120

QY 121 LNQASLRPMQRGKLVLTNLNCOLVVEBGRVRAMAARSLSRGLERTVTELLOHONPOOLSANL 180
121 LNQASLRPMQRGKLVLTNLNCOLVVEBGRVRAMAARSLSRGLERTVTELLOHONPOOLSANL 180

QY 181 WAAVRARGCQFLGPMQEAALKLVLAEDSALSRSKVLVFLVQBLERPPRQASKTSG 240
181 WAAVRARGCQFLGPMQEAALKLVLAEDSALSRSKVLVFLVQBLERPPRQASKTSG 240

QY 301 SSILYGDLAHKSHMOSIDKLQSPESPAKSVOBLTIVLORTGPANLNRPHLELLANI 360
301 SSILYGDLAHKSHMOSIDKLQSPESPAKSVOBLTIVLORTGPANLNRPHLELLANI 360

Db 301 SSILYGLAHKSHMOSIDIKLQSPESFAKSQVBLTIVLQRGPANLNLRPHLEJANI 360 ; SEQ ID NO 22109
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-452-680-22109
; Query Match 100.0%; Score 6215; DB 49; Length 1191;
; Best Local Similarity 100 %; Pred. No. 0;
; Matches 1191; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
; Matches 1191; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
; Db 361 DPNPDAVSPTWEOLENAMAVAKTVVHGLDVRIONYSRKGHETPOPONSKTYKTSMDLR 420
; 421 QGGCPRGTNCFAHSOELEKYLRNKKINATVRFLPLANKGVVNNTTTAGNIVI 480
; 421 QGGCPRGTNCFAHSOELEKYLRNKKINATVRFLPLANKGVVNNTTTAGNIVI 480
; Qy 481 GSTETGKIVSTNGSNAENSVQLRSSTDRALETWKVGKANGONAGPSAD 540
; 481 GSTETGKIVSTNGSNAENSVQLRSSTDRALETWKVGKANGONAGPSAD 540
; Qy 541 SVTENKIGSPPKTPVSNVAATSAGPSNGTELSVQOKSSPLTRPVVYPHSENQFO 600
; 541 SVTENKIGSPPKTPVSNVAATSAGPSNGTELSVQOKSSPLTRPVVYPHSENQFO 600
; Db 541 SVTENKIGSPPKTPVSNVAATSAGPSNGTELSVQOKSSPLTRPVVYPHSENQFO 600
; 601 DPRTOIPPEVQYQPGYPPPTVAGVACCVPPRFRNVPESLPPASMPYADYST 660
; 601 DPRTOIPPEVQYQPGYPPPTVAGVACCVPPRFRNVPESLPPASMPYADYST 660
; Qy 661 FSPRDMMSSYQPPRQPKVDPVPPSGMAYAPVDSRTRWPPMQRDDITRSLNLP 720
; 661 FSPRDMMSSYQPPRQPKVDPVPPSGMAYAPVDSRTRWPPMQRDDITRSLNLP 720
; Db 661 FSPRDMMSSYQPPRQPKVDPVPPSGMAYAPVDSRTRWPPMQRDDITRSLNLP 720
; 721 DMHSSVYQTSLRERYNLDGYSYACOPSPSPRTVPLPRCPGHLKTSCEQIRRKPD 780
; 721 DMHSSVYQTSLRERYNLDGYSYACOPSPSPRTVPLPRCPGHLKTSCEQIRRKPD 780
; Db 721 DMHSSVYQTSLRERYNLDGYSYACOPSPSPRTVPLPRCPGHLKTSCEQIRRKPD 780
; 781 QWAQYHTOKAPLVSLPVATOSPTPSPLSVDFRADSFBSVSGTKFEEDHLSHSPWS 840
; 781 QWAQYHTOKAPLVSLPVATOSPTPSPLSVDFRADSFBSVSGTKFEEDHLSHSPWS 840
; Db 840 QWAQYHTOKAPLVSLPVATOSPTPSPLSVDFRADSFBSVSGTKFEEDHLSHSPWS 840
; 901 IISKGMAISRSRTGHTTDPVQATASQGATKPSVSDVYVNAVDSRWSYNEATS 960
; 901 IISKGMAISRSRTGHTTDPVQATASQGATKPSVSDVYVNAVDSRWSYNEATS 960
; Db 901 IISKGMAISRSRTGHTTDPVQATASQGATKPSVSDVYVNAVDSRWSYNEATS 960
; 961 SAHYVERDRFTWDGHRKHSSTGDLISLQOAKNSLIOREANALAMQKNSLDE 1020
; 961 SAHYVERDRFTWDGHRKHSSTGDLISLQOAKNSLIOREANALAMQKNSLDE 1020
; Db 1020 SAHYVERDRFTWDGHRKHSSTGDLISLQOAKNSLIOREANALAMQKNSLDE 1020
; 1021 GRHLTNLISLKEIELRNGELOSSDYTEDATKRDIELELSALDTDEQSERIEEL 1080
; 1021 GRHLTNLISLKEIELRNGELOSSDYTEDATKRDIELELSALDTDEQSERIEEL 1080
; Db 1080 DIOLGISSONQDQOLLNGMAVENQHPVQHQKEPKPKQKQSGLBDHVILEQTLTLPVSCF 1140
; 1080 DIOLGISSONQDQOLLNGMAVENQHPVQHQKEPKPKQKQSGLBDHVILEQTLTLPVSCF 1140
; Db 1141 SOPLPVYSISACSLCLPITSVAGNLILKTHYNSEDKNDFLKEVANGRMNS 1191
; 1141 SOPLPVYSISACSLCLPITSVAGNLILKTHYNSEDKNDFLKEVANGRMNS 1191
; Db 1141 SOPLPVYSISACSLCLPITSVAGNLILKTHYNSEDKNDFLKEVANGRMNS 1191
; RESULT 3
; US-60-452-680-22109
; Sequence 22109, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/452, 680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSEQ for Windows Version 4.0

RESULT 4
 US-60-453-050-13599
 ; Sequence 13599, Application US/60453050
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: LUKE, May
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001457
 ; CURRENT APPLICATION NUMBER: US/60/453, 050
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 13599
 ; LENGTH: 1191
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-453-050-13599

Query Match 100 %; Score 6215; DB 49; Length 1191;
 Best Local Similarity 100 %; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVQAQWTERTEFLSCPICYCNEFEDENVHKPISLUGCSHTVKCTCLNKLKRAACPFDOTAINTD 60
 1 MPVQAQWTERTEFLSCPICYCNEFEDENVHKPISLUGCSHTVKCTCLNKLKRAACPFDOTAINTD 60

Db 61 IDVLPYNFAILQLQVGAQYDPSIKLSNLGENKHYEVAKCCKEDALYLKPSLGKGVAS 120
 61 IDVLPYNFAILQLQVGAQYDPSIKLSNLGENKHYEVAKCCKEDALYLKPSLGKGVAS 120

Db 61 IDVLPYNFAILQLQVGAQYDPSIKLSNLGENKHYEVAKCCKEDALYLKPSLGKGVAS 120

QY 121 LNQSLASRPMQRKLVLTUNQVEECVRAMARSLGERVTTELILQHNPQLSANL 180
 121 LNQSLASRPMQRKLVLTUNQVEECVRAMARSLGERVTTELILQHNPQLSANL 180

Db 181 WAAVRARGCQFQGPAMOBEALKVLVLAEDGSSALSRSKVLVIFVVQBLEPREFOASKTSIG 240
 181 WAAVRARGCQFQGPAMOBEALKVLVLAEDGSSALSRSKVLVIFVVQBLEPREFOASKTSIG 240

QY 241 HVVOLYTRASCKVTKREDDESSIMOLKEFRSYEARREHQDQVIVIAMEAGLTSPEQW 300
 241 HVVOLYTRASCKVTKREDDESSIMOLKEFRSYEARREHQDQVIVIAMEAGLTSPEQW 300

Db 301 SLLYGLAHKSHMOSIDKQSPESAKSVQELTIVQRTDPANLRPPELLANT 360
 301 SLLYGLAHKSHMOSIDKQSPESAKSVQELTIVQRTDPANLRPPELLANT 360

QY 361 DPNPDAVSPTWOLENAMAVVTVVHLVDFIONYRKHFTQPQPNSKKTSMDRL 420
 361 DPNPDAVSPTWOLENAMAVVTVVHLVDFIONYRKHFTQPQPNSKKTSMDRL 420

Db 421 QGGCGRGTCTCAHSOBELLEYKLRKKINATVRTPPLNKVGVNNTTTAGNTIVSI 480
 421 QGGCGRGTCTCAHSOBELLEYKLRKKINATVRTPPLNKVGVNNTTTAGNTIVSI 480

QY 541 SVTENKIGSPPKTPSVNAATSAGSNSVQLSRSTDSTURALETYKKGANGONAAGPSAD 540
 541 SVTENKIGSPPKTPSVNAATSAGSNSVQLSRSTDSTURALETYKKGANGONAAGPSAD 540

Db 541 DPTOIPFEVPOYPOGYRPPTVAGWAPCVPRVRSNVPESLPPRASMPYADYST 660
 541 DPTOIPFEVPOYPOGYRPPTVAGWAPCVPRVRSNVPESLPPRASMPYADYST 660

Db 601 DPTQIPFEVPOQYQPGYYPPTVAGWAPCVPRVRSNVPESLPPRASMPYADYST 660
 601 DPTQIPFEVPOQYQPGYYPPTVAGWAPCVPRVRSNVPESLPPRASMPYADYST 660

Db 661 FSPRMNNSSPYQPPQPPQYGPVPPVPSGMAYPVDSRIRWRPPMFTODDLIRNSLPM 720
 661 FSPRMNNSSPYQPPQPPQYGPVPPVPSGMAYPVDSRIRWRPPMFTODDLIRNSLPM 720

Db 721 DVMHSSVYQTSRERYNSLOGYSYACOPSEPRTRVPLPREPCGHLKSCBQRRKD 780
 721 DVMHSSVYQTSRERYNSLOGYSYACOPSEPRTRVPLPREPCGHLKSCBQRRKD 780

Db 781 QWAQHTOKAPLVSSLPPVATOSPTPPSPLFSVDPRADFSVSUSGTKEEDHLSYSPWS 840
 781 QWAQHTOKAPLVSSLPPVATOSPTPPSPLFSVDPRADFSVSUSGTKEEDHLSYSPWS 840

Db 841 CGTISCINAIIDSEPKDVIAINSVAMLDQSGDVKRVRVHFETORTKEDP1PFSDGP 900
 841 CGTISCINAIIDSEPKDVIAINSVAMLDQSGDVKRVRVHFETORTKEDP1PFSDGP 900

Db 901 IISKWGAISRSRTGHTPVQATASQGATKPIVSVDVYPUVYNAVDSRWSSYNEATS 960
 901 IISKWGAISRSRTGHTPVQATASQGATKPIVSVDVYPUVYNAVDSRWSSYNEATS 960

Db 961 SAHYVERDRFTVTDLSGHRHSSTGDLISLBLOQAKNSNLLQREANALAMQKNSLDE 1020
 961 SAHYVERDRFTVTDLSGHRHSSTGDLISLBLOQAKNSNLLQREANALAMQKNSLDE 1020

Db 1021 GRHLTNLNSKEIELRNGELOSDYTEDATDKPDRDIELELSALDTDEPDQSEBEEIL 1080
 1021 GRHLTNLNSKEIELRNGELOSDYTEDATDKPDRDIELELSALDTDEPDQSEBEEIL 1080

Db 1081 DIQLGSSONDOLLNGMAVENGHPYQOHQKPKQKQKSLEDGHVILEEQTILPVTSFC 1140
 1081 DIQLGSSONDOLLNGMAVENGHPYQOHQKPKQKQKSLEDGHVILEEQTILPVTSFC 1140

Db 1141 SQPLPVISNASCLPITSVAGNLILKTHMSEDKFLKPVANGKVN 1191
 1141 SQPLPVISNASCLPITSVAGNLILKTHMSEDKFLKPVANGKVN 1191

RESULT 5
 US-60-453-135-13599
 ; Sequence 13599, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: TAKOBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001456
 ; CURRENT APPLICATION NUMBER: US/60/453, 135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 13599
 ; LENGTH: 1191
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-453-135-13599

Query Match 100 %; Score 6215; DB 49; Length 1191;
 Best Local Similarity 100 %; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPVQAQWTERFLSCPICYCNEFEDENVHKPISLUGCSHTVKCTCLNKLKRAACPFDOTAINTD 60

Db 1 MPVQAAQWTERFISCPICYNEFDENVKPIISLGCSHTVCKTCUNKLHKACFPQTINTD 60
 Qy 61 IDVLVPNFALLQVGAQVDPDQHOSIKLSNLGENKHYEVAKKCVEDLALYLKLPSGGKVAS 120
 Db 61 IDVLVPNFALLQVGAQVDPDQHOSIKLSNLGENKHYEVAKKCVEDLALYLKLPSGGKVAS 120
 Qy 121 LNQSALSRPMQRKVLTNLNCOLVEEGRRVRAAALSGLGERTVTETLQHONPQLSANL 180
 Db 121 LNQSALSRPMQRKVLTNLNCOLVEEGRRVRAAARSGLGERTVTETLQHONPQLSANL 180
 Qy 181 WAAVRARGCQFLGPAMQEEALKVLVLALEDGALSRSKVLVFVQRLERPPQASKTIG 240
 Db 181 WAAVRARGCQFLGPAMQEEALKVLVLALEDGALSRSKVLVFVQRLERPPQASKTIG 240
 Qy 241 HVVOLYRASCFKVTKRDEDSIMOLKEFESYEARREHDQAQVITAMEAGLRSPEQW 300
 Db 241 HVVOLYRASCFKVTKRDEDSIMOLKEFESYEARREHDQAQVITAMEAGLRSPEQW 300
 Qy 301 SLLYGDLAHKSHMOSITDKLQSPESFAKSVOBLTIVLQRTGDPANLNLRPHLEIANI 360
 Db 301 SLLYGDLAHKSHMOSITDKLQSPESFAKSVOBLTIVLQRTGDPANLNLRPHLEIANI 360
 Qy 361 DPNPDAVSPTWOLENAMAVKTVVAGLVDITQNSRKGHTPOPDKTSKMTSMDR 420
 Db 361 DPNPDAVSPTWOLENAMAVKTVVAGLVDITQNSRKGHTPOPDKTSKMTSMDR 420
 Qy 421 QGGCGRGTNTFAHSQEELKYLRLNNKINATVRTPPLNKVGVNNTTTAGNTISVI 480
 Db 421 QGGCGRGTNTFAHSQEELKYLRLNNKINATVRTPPLNKVGVNNTTTAGNTISVI 480
 Qy 481 GSTETGKIVSTNGISNAENSVSOLRSRSTDSTLRALETWTKVKVGANGONAGPSAD 540
 Db 481 GSTETGKIVSTNGISNAENSVSOLRSRSTDSTLRALETWTKVKVGANGONAGPSAD 540
 Qy 541 SVTENKIGSPPKTPVNSVAASAGPSNGTENSLVQSSFLTRIPVYPPHSENTOYQO 600
 Db 541 SVTENKIGSPPKTPVNSVAASAGPSNGTENSLVQSSFLTRIPVYPPHSENTOYQO 600
 Qy 601 DPTQIPFEVPOQYPOQTYYPPTVPGAVCPVPRVSNNNPPESLPPASMPYADYST 660
 Db 601 DPTQIPFEVPOQYPOQTYYPPTVPGAVCPVPRVSNNNPPESLPPASMPYADYST 660
 Qy 661 FSPDRMNSSPPQPPPQYPPVPPSGMAPPVYDSRTRRPPMQRDDITRSLPPM 720
 Db 661 FSPDRMNSSPPQPPPQYPPVPPSGMAPPVYDSRTRRPPMQRDDITRSLPPM 720
 Db 601 DPTQIPFEVPOQYPOQTYYPPTVPGAVCPVPRVSNNNPPESLPPASMPYADYST 660
 Qy 721 DVMHSSSYTTSRERTNSLDGYSYVACQPSSEPRPTVPLPREGCHIKTSEECCRKD 780
 Db 721 DVMHSSYTTSRERTNSLDGYSYVACQPSSEPRPTVPLPREGCHIKTSEECCRKD 780
 Qy 781 QWAQYHTOKAPVSVSTLPVATOQTPPSPLSVDFRADFSESSVSGTRFEEDLSHYSPWS 840
 Db 841 CGTIGSCINAIDSEPKDVIANVAMLDGSDVKRVLHFTTORTEKEBPIPFSDPG 900
 Db 841 CGTIGSCINAIDSEPKDVIANVAMLDGSDVKRVLHFTTORTEKEBPIPFSDPG 900
 Db 781 QWAQYHTOKAPVSVSTLPVATOQTPPSPLSVDFRADFSESSVSGTRFEEDLSHYSPWS 840
 Qy 901 IISKWMAISRSSTGHTTDQVATOSGSAKPLSUDVYTFYNAVDRSRSISHEATS 960
 Db 901 IISKWMAISRSSTGHTTDQVATOSGSAKPLSUDVYTFYNAVDRSRSISHEATS 960
 Qy 961 SAWYVERDFTDLSCHRHSSTGDLISLHQAKNSNLJLQREANALAMQWNSLDE 1020
 Db 961 SAWYVERDFTDLSCHRHSSTGDLISLHQAKNSNLJLQREANALAMQWNSLDE 1020
 Qy 961 SAWYVERDFTDLSCHRHSSTGDLISLHQAKNSNLJLQREANALAMQWNSLDE 1020
 Db 1021 GRHLTNLISKEIELNGELOGSDYTEDATTPRDTELETSALDTDEPGQSEPEBIL 1080
 Qy 1021 GRHLTNLISKEIELNGELOGSDYTEDATTPRDTELETSALDTDEPGQSEPEBIL 1080
 Db 1021 GRHLTNLISKEIELNGELOSSDYTEADTPRDTELETSALDTDEPGQSEPEBIL 1080
 Qy 1081 DOLGIGSISONDOLLINGWAVENGHPVOCOKRSPKKQKSLGRDHVILEBQKILPTSCF 1140

Db 1081 DOLGIGSISONDOLLINGWAVENGHPVOCOKRSPKKQKSLGRDHVILEBQKILPTSCF 1140
 Qy 1141 S0PLPVISNASCLOPITSVAGNLKTAHMSDKNFLKPVANGKVNNS 1191
 Db 1141 S0PLPVISNASCLOPITSVAGNLKTAHMSDKNFLKPVANGKVNNS 1191
 RESULT 6
 US-60-466-412-13599
 ; Sequence 13599, Application US/60466412
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C101466
 ; CURRENT APPLICATION NUMBER: US/60/466, 412
 ; CURRENT FILING DATE: 2003-04-30
 ; NUMBER OF SEQ ID NOS: 429241
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 13599
 ; LENGTH: 1191
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-466-412-13599
 Query Match 100 %; Score 6215; DB 49; Length 1191;
 Best Local Similarity 100 %; Pred. No. 0;
 Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MPVQAAQWTERFISCPICYNEFDENVKPIISLGCSHTVCKTCUNKLHKACFPQTINTD 60
 Db 1 MPVQAAQWTERFISCPICYNEFDENVKPIISLGCSHTVCKTCUNKLHKACFPQTINTD 60
 Qy 61 IDVLVPNFALLQVGAQVDPDQHOSIKLSNLGENKHYEVAKKCVEDLALYLKLPSGGKVAS 120
 Db 61 IDVLVPNFALLQVGAQVDPDQHOSIKLSNLGENKHYEVAKKCVEDLALYLKLPSGGKVAS 120
 Qy 121 LNQSALSRPMQRKVLTNLNCOLVEEGRRVRAAALSGLGERTVTETLQHONPQLSANL 180
 Db 121 LNQSALSRPMQRKVLTNLNCOLVEEGRRVRAAARSGLGERTVTETLQHONPQLSANL 180
 Qy 181 WAAVRARGCQFLGPAMQEEALKVLVLALEDGALSRSKVLVFVQRLERPPQASKTIG 240
 Db 181 WAAVRARGCQFLGPAMQEEALKVLVLALEDGALSRSKVLVFVQRLERPPQASKTIG 240
 Qy 241 HVVOLYRASCFKVTKRDEDSIMOLKEFESYEARREHDQAQVITAMEAGLRSPEQW 300
 Db 241 HVVOLYRASCFKVTKRDEDSIMOLKEFESYEARREHDQAQVITAMEAGLRSPEQW 300
 Qy 301 SLLYGDLAHKSHMOSITDKLQSPESFAKSVOBLTIVLQRTGDPANLNLRPHLEIANI 360
 Db 301 SLLYGDLAHKSHMOSITDKLQSPESFAKSVOBLTIVLQRTGDPANLNLRPHLEIANI 360
 Qy 361 DPNPDAVSPTWOLENAMAVKTVVAGLVDITQNSRKGHTPOPDKTSKMTSMDR 420
 Db 361 DPNPDAVSPTWOLENAMAVKTVVAGLVDITQNSRKGHTPOPDKTSKMTSMDR 420
 Qy 421 QGGCGRGTNTFAHSQEELKYLRLNNKINATVRTPPLNKVGVNNTTTAGNTISVI 480
 Db 421 QGGCGRGTNTFAHSQEELKYLRLNNKINATVRTPPLNKVGVNNTTTAGNTISVI 480
 Qy 481 GSTETGKIVSTNGISNAENSVSOLRSRSTDSTLRALETWTKVKVGANGONAGPSAD 540
 Db 541 SVTENKIGSPPKTPVNSVAASAGPSNGTENSLVQSSFLTRIPVYPPHSENTOYQO 600
 Db 601 DPTQIPFEVPOQYPOQTYYPPTVPGAVCPVPRVSNNNPPESLPPASMPYADYST 660

RESULT 7

US-10-619-992-4

; Sequence 4, Application US/10619992

; GENERAL INFORMATION:

; APPLICANT: Refenseder, Steven

; APPLICANT: Merkins, Louise

; APPLICANT: Bennett, Robert

; APPLICANT: Seiss, Donald

TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene

FILE REFERENCE: 00-617-A

CURRENT APPLICATION NUMBER: US/10/619,992

CURRENT FILING DATE: 2003-07-15

PRIOR APPLICATION NUMBER: US/09/921,099

PRIOR FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 1191

TYPE: PRT

ORGANISM: Homo sapiens

US-10-619-992-4

Query Match 99.9% Score 6207; DB 36; Length 1191;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 1190; Conservative 0;

1 MPVQAAQWTEFSCPICYNEFEDENHVKPISLCSHTVKTCINKLKLKACPFQDQTAINTD 60

1 MAVOQAQWTEFSCFCYNEFEDENHVKPISLCSHTVKTCINKLKLKACPFQDQTAINTD 60

61 DVULPVNFAFLQVLGAQVDPHQSKLUSNLGENKHYEAKCVEDALYKLGSLGGKGVAS 120

61 DVULPVNFAFLQVLGAQVDPHQSKLUSNLGENKHYEAKCVEDALYKLGSLGGKGVAS 120

121 LNQSA1SLRPMQRKLVTLVNCOLVVEGRVRMARAISLGERTVTTELQHONPOOLSNL 180

Db 121 LNQSA1SLRPMQRKLVTLVNCOLVVEGRVRMARAISLGERTVTTELQHONPOOLSNL 180

Qy 181 WAAVRARGCQTIGPAMQEAEALKVLAEGSALSRSRKVLFVWQLEPRFPOAKSTIG 240

Db 181 WAARVARGCQLGRPMQEAELKVKVLAEGSALSRSRKVLFVWQLEPRFPOAKSTIG 240

Db 241 HVVQLYRASCFKVTRKDSSLMQKEFRSYEARREHDQVHIAAMBGLRSPQW 300

Qy 241 HVVQLYRASCFKVTRKDSSLMQKEFRSYEARREHDQVHIAAMBGLRSPQW 300

Db 301 SSILYCDLAHKSHMOSIDKLQSPESPAKSYOELTIVLQRTGDPANLNRLRPHELLANI 360

Qy 301 SSILYCDLAHKSHMOSIDKLQSPESPAKSYOELTIVLQRTGDPANLNRLRPHELLANI 360

Db 361 DPNPDAVSPTMEQLENNAMAVAKTVHGLVUPTQOPNPKYTKSMCRDLR 420

Qy 361 DPNPDAVSPTMEQLENNAMAVAKTVHGLVUPTQOPNPKYTKSMCRDLR 420

Db 361 DPNPDAVSPTMEQLENNAMAVAKTVHGLVUPTQOPNPKYTKSMCRDLR 420

Qy 421 QOGGCPRGNTPAHSQEBLKYLANKINATVRTFPPLNKVGUNNTTTAGNIVI 480

Db 421 QOGGCPRGNTPAHSQEBLKYLANKINATVRTFPPLNKVGUNNTTTAGNIVI 480

Qy 481 GSTETTGKIVPSTNGISNAENSVSOLISRSDTSTRALETTVKVGKGANGQNAAGPSAD 540

Db 481 GSTETTGKIVPSTNGISNAENSVSOLISRSDTSTRALETTVKVGKGANGQNAAGPSAD 540

Qy 541 SVTENKIGSPKTPYPSVNAATSAGSNSNGVTELNSPQKSPLTRPVYPYPPHENIQFO 600

Db 541 SVTENKIGSPKTPYPSVNAATSAGSNSNGVTELNSPQKSPLTRPVYPYPPHENIQFO 600

Qy 601 DPRTOIPFEVQYPOGYPPPTVAGVAPCVPRVRNNVPSSLPASMPYADYST 660

Db 601 DPRTOIPFEVQYPOGYPPPTVAGVAPCVPRVRNNVPSSLPASMPYADYST 660

Qy 661 FSPDRMNNSPYOPPPQPGVPPVPGM*APVUDSRIRWPPMQRDDIIRSNSLPP 720

Db 661 FSPDRMNNSPYOPPPQPGVPPVPGM*APVUDSRIRWPPMQRDDIIRSNSLPP 720

Qy 722 DVMHSSVYQTSLERNSLDCCYYSVACQPSEPRTTVPLPREPCGHILKTSEBQIRKPD 780

Db 722 DVMHSSVYQTSLERNSLDCCYYSVACQPSEPRTTVPLPREPCGHILKTSEBQIRKPD 780

Qy 781 QWAQHQTOKAIVLVSSTLPTAVOSPTPSPLSVDFRADFSVSGTKFEEDHLHSPWS 840

Db 781 QWAQHQTOKAIVLVSSTLPTAVOSPTPSPLSVDFRADFSVSGTKFEEDHLHSPWS 840

Qy 841 CGTIGSCINAIDSEPKDVIANSNAMLDQGDVKERVHFETQRTEKEPIIPSDGP 900

Db 841 CGTIGSCINAIDSEPKDVIANSNAMLDQGDVKERVHFETQRTEKEPIIPSDGP 900

Qy 901 ITSKWGA1SRSRSGRTGHTDPQATASQGSAKTPISVSDYPPYVNAVDSRNSYGEATS 960

Db 901 ITSKWGA1SRSRSGRTGHTDPQATASQGSAKTPISVSDYPPYVNAVDSRNSYGEATS 960

Qy 961 SAHYVERDRFTVTDLSGRKHSSTGDLISLEQAKNSLLOREANALAMQKWNLD 1020

Db 961 SAHYVERDRFTVTDLSGRKHSSTGDLISLEQAKNSLLOREANALAMQKWNLD 1020

Qy 1021 GRHLTNLISKEBLRNGELOSQDYTEDATDKPDRDELSALDTDPDQSEPIFEEL 1080

Db 1021 GRHLTNLISKEBLRNGELOSQDYTEDATDKPDRDELSALDTDPDQSEPIFEEL 1080

Qy 1081 DOLGQSSQNDOQLNGMAVENGPVQOHQKEPPKQKQSLGDBHVTLEQKTYLPTVTSF 1140

Db 1081 DOLGQSSQNDOQLNGMAVENGPVQOHQKEPPKQKQSLGDBHVTLEQKTYLPTVTSF 1140

Qy 1141 SQPLPVSIASACLPTTSVSVAGNLKTHMSEKNDFLKPVANGKVN 1191

Db 1141 SQPLPVSIASACLPTTSVSVAGNLKTHMSEKNDFLKPVANGKVN 1191

121 LNQSA1SLRPMQRKLVTLVNCOLVVEGRVRMARAISLGERTVTTELQHONPOOLSNL 180

US-60-243-734-16

; Sequence 16, Application US/60243734

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING

; PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

; TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF

; FILE REFERENCE: CLO00932

; CURRENT APPLICATION NUMBER: US/60/243,734

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSEQ For Windows Version 4.0

; SEQ ID NO: 16

; LENGTH: 1137

; TYPE: PRT

; ORGANISM: HUMAN

; US-60-243-734-16

Query Match 94.6%; Score 5880; DB 47; Length 1137;

Best Local Similarity 95.4%; Pred. No. 0; Mismatches 0; Indels 54; Gaps 3;

Matches 1136; Conservative 1;

; Qy

1 MPVOQALQWTERESPCLCYNEFDEPVENVKPISCGCSHTVKCTINKLHKACPFDTAINTD 60

2 MPVOQALQWTERESPCLSPCICYNEFDEPVENVKPISLGCSHTVKCTINKLHKACPFDTAINTD 60

3 MPVOQALQWTERESPCLSPCICYNEFDEPVENVKPISLGCSHTVKCTINKLHKACPFDTAINTD 60

4 MPVOQALQWTERESPCLSPCICYNEFDEPVENVKPISLGCSHTVKCTINKLHKACPFDTAINTD 60

51 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

61 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

62 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

63 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

64 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

65 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

66 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

67 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

68 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

69 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

70 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

71 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

72 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

73 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

74 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

75 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

76 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

77 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

78 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

79 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

80 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

81 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

82 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

83 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

84 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

85 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

86 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

87 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

88 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

89 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

90 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

91 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

92 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

93 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

94 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

95 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

96 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

97 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

98 IDVLPLPNFALQVLGAQVDPHQSIKUSNLGENKHYEAKKVEDALYLKPLSGGKVAS 120

Qy

781 QWAQHTQAKPLVSSTLPVATQSPTTSPFLPSVDRADFSRSVSGTKFEPDHLHSPWS 840

792 QWAQHTQAKPLVSSTLPVATQSPTTSPFLPSVDRADFSRSVSGTKFEPDHLHSPWS 800

793 CGTIGSCINAIIDSEPKDVILVANSNAVIMDLQGDVVERVHIFETORTKEEDPLIPSDG 900

801 CGTIGSCINAIDSEPKDVILVANSNAVIMDLQGDVVERVHIFETORTKEEDPLIPSDG 860

802 IISKWGAISRSRSRTGHTDVOQATASQGSATKPSVSYVPAVNDSRVSSYGEATS 960

803 IISKWGAISRSRSRTGHTDVOQATASQGSATKPSVSYVPAVNDSRVSSYGEATS 920

804 SAHYVERDRFTVTDLSGHKRSSTSGLSLBLQOKNSLILQOREANALAMQKNSLIDE 1020

805 921 SAHYVE-----RKHSSTGDLISLBLQOKNSLILQOREANALAMQKNSLIDE 968

806 1021 GRHTNLISKEIERNGELOSDYTEDATKPRDIELSALDTPDQCOSEPIEL 1080

807 969 GRHHTNLISKEIELRNGE-SDYTEDATDTPRDPDIELSALDTPDQSERIEEL 1026

808 1081 DIOLGISSONDOLLNGMAVENGHPVQOHQEKEPPQCKQSGCGBDHVILEBEQKTLPTVSC 1140

810 1027 DIOLGISSONDOLLNGMAVENGHPVQOHQEKEPPQCKQSGCGBDHVILEBEQKTLPTVSC 1086

811 1141 SQPLPVISINASCLPITTSVSGNLTIKTMSEDKFLKPVANGKVN 1191

812 1087 SQPLPVISINASCLPITTSVSGNLTIKTMSEDKFLKPVANGKVN 1137

RESULT 9

US-10-170-205E-29971

; Sequence 29971, Application US/10170205E

; GENERAL INFORMATION:

; APPLICANT: ADAMS, Mark

; TITLE OF INVENTION: DEVICES SUCH AS ARRAYS, COMPRISING OF HUMAN PROTEINS OR PROTEIN

; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

; FILE REFERENCE: CLO01381

; CURRENT APPLICATION NUMBER: US/10/170,209E

; CURRENT FILING DATE: 2002-06-13

; NUMBER OF SEQ ID NOS: 40312

; SOFTWARE: Patentin version 3.2

; SEQ ID NO: 29971

; LENGTH: 1062

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-170-205E-29971

Query Match 88.9%; Score 5529; DB 31; Length 1062;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1062; Conservative 0;

; Qy

130 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

131 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

132 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

133 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

134 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

135 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

136 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

137 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

138 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

139 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

140 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

141 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

142 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

143 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

144 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

145 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

146 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

147 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

148 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

149 MORKLUTLVLNCOLVERBERGRVRAARSGLERTVTELLQLVLPNQOOLNPOOLQNSLNLWAVERGRC 189

150 SCPKVTKRDESSLQMIKEERSYEARRHDQIAVHIMAMEAGRLISPEQOMSLLYGDLA 309

151 SCPKVTKRDESSLQMIKEERSYEARRHDQIAVHIMAMEAGRLISPEQOMSLLYGDLA 309

Qy

181 HKSHMOSIIDLQSPSFPAKSVOELTIVLQRTGDPANLNRPHLILLANIDPNPDAWP 240

182 121 SCFKVTKRDESSLQMIKEERSYEARRHDQIAVHIMAMEAGRLISPEQOMSLLYGDLA 180

183 310 HKSHMOSIIDLQSPSFPAKSVOELTIVLQRTGDPANLNRPHLILLANIDPNPDAWP 369

184 61 OPLGPAMQOEALKLVILLEADGSALSRSRKVLFLVWORLERPPOASKTSIGHVOLYRA 120

185 250 SCPKVTKRDESSLQMIKEERSYEARRHDQIAVHIMAMEAGRLISPEQOMSLLYGDLA 309

186 122 SCFKVTKRDESSLQMIKEERSYEARRHDQIAVHIMAMEAGRLISPEQOMSLLYGDLA 180

187 370 TWEOLENAMAVAKTVVHGLVPFIQNSRKGHTPOQPNKSYTSMCRDLRQGGCPRT 429

188 241 TWEOLENAMAVAKTVVHGLVPFIQNSRKGHTPOQPNKSYTSMCRDLRQGGCPRT 300

189 430 NCTFAHSQEELEYKLRNKKINATVTFPLNKVGVNNTVTTAGNVISVIGSTETGKI 489

	Matches	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Db	301	NCTFAHSQEELEYKYLNRNKKNATRTPLINKGVNTNTVTTAGNVISIGSTETGKI	360						
Qy	490	VPTNGISNAENSVSOLISRSSTDSTRALETVKKVKGANGQNAAGPSADSVTENKIGS	549						
Db	361	VPSTNGISNAENSVSOLISRSSTDSTRALETVKKVKGANGQNAAGPSADSVTENKIGS	420						
Qy	550	PPKTPVSNVAATSAGPSNVGTELNSVPOQSSPFLTRVPPPHSENIOYFQDPRTOIPE	609						
Db	421	PPKTPVSNVAATSAGPSNVGTELNSVPOQSSPFLTRVPPPHSENIOYFQDPRTOIPE	480						
Qy	610	VHQYRQGTYPPPTVPGAVACPVPRFRSNVPESSLPPASMPYADHYSTSPRDMS	669						
Db	481	VHQYRQGTYPPPTVPGAVACPVPRFRSNVPESSLPPASMPYADHYSTSPRDMS	540						
Qy	670	SPYQPPPPQGPVPPVPGAVACPVPRFRSNVPESSLPPASMPYADHYSTSPRDMS	729						
Db	541	SPYQPPPPQGPVPPVPGAVACPVPRFRSNVPESSLPPASMPYADHYSTSPRDMS	540						
Db	541	SPYQPPPPQGPVPPVPGAVACPVPRFRSNVPESSLPPASMPYADHYSTSPRDMS	600						
Qy	730	TSLERYNLSLDGGYSYACQPSSEPRTVPLPRECPCHLKUSCEEQTRRKPDQWAQHTQ	789						
Db	601	TSLERYNLSLDGGYSYACQPSSEPRTVPLPRECPCHLKUSCEEQTRRKPDQWAQHTQ	660						
Qy	790	APLVSSTPVATQSPPSPSPLSFVDRADFSBSVSQTKFEEDHLSYSPSCGTGSCIN	849						
Db	661	AIDSEPKDVIANSAVLMDSGDVKRVRHETQRRTKEEDIPIIPSDGIIISKWGAIS	909						
Db	721	AIDSEPKDVIANSAVLMDSGDVKRVRHETQRRTKEEDIPIIPSDGIIISKWGAIS	780						
Qy	910	RSSRTGHTTPVQATASQGATKPSVSDVPPVYNAVDSRNSYGNBATESSAHYVERD	969						
Db	781	RSSRTGHTTPVQATASQGATKPSVSDVPPVYNAVDSRNSYGNBATESSAHYVERD	840						
Qy	970	FIVTDLSGRKRHSSTGDLSLBLQQAKNSNLLOREANALAMQKNSLDGRHLTTNL	1029						
Db	841	FIVTDLSGRKRHSSTGDLSLBLQQAKNSNLLOREANALAMQKNSLDGRHLTTNL	900						
Qy	1030	SKEIELRNGELOSODYTADTKPDRDELESLALDTDEPQOSEPIEIDIOLGISSQ	1089						
Db	901	SKEIELRNGELOSODYTADTKPDRDELESLALDTDEPQOSEPIEIDIOLGISSQ	960						
Qy	1090	NDQLLNGMAVENGHPVQOHOKEPPKOKQSLGEDHVILEQKTLIPTSCSQPLVIS	1149						
Db	961	NDQLLNGMAVENGHPVQOHOKEPPKOKQSLGEDHVILEQKTLIPTSCSQPLVIS	1020						
Db	1150	NASCLPITTSVAGNLILKTHMSEDKNDFLKVANGKMVIS	1191						
Db	1021	NASCLPITTSVAGNLILKTHMSEDKNDFLKVANGKMVIS	1062						
RESULT	10								
US-60-452-680-22108									
; Sequence 22108 Application US/60452680									
; GENERAL INFORMATION:									
; APPLICANT: CARGILL, Michele									
; APPLICANT: GRUPE, Andrew									
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH									
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF									
; FILE REFERENCE: CI001450									
; CURRENT APPLICATION NUMBER: US/60/452,680									
; CURRENT FILING DATE: 2003-03-07									
; NUMBER OF SEQ ID NOS: 116213									
; SOFTWARE: FastSEQ for Windows Version 4.0									
; SEQ ID NO 22108									
; LENGTH: 1062									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-60-452-680-22108									
Query Match	88.9%	Score 5525;	DB 49;	Length 1062;					
Best Local Similarity	100.0%	Score 5525;	DB 49;	Length 1062;					

Db 1 MQRKLVTLLVNCOLVNEBEGVRAMRAARSGLGRTVTBLILQHQNQQLSALNLAVERGC 60
 Db 361 VESTNGTISNAENSVSQSLISRSTDSTRLAETVKKGKVGANGQNAAGPSADSUTENKIGS 420
 Qy 550 PPKTPVSNAATTSAGSNVNGTELNSPKQSSPFLTRPVPPHSENIOYFQDPRTQIPFE 609
 Db 421 PPKTPVSNAATTSAGSNVNGTELNSPKQSSPFLTRPVPPHSENIOYFQDPRTQIPFE 480
 Qy 610 VPQYPTQGYPPPTVPGAVCPVPRVRSNNVPESLPPASMPYADHYSFTSPDRMNS 669
 Db 481 VPQYPTQGYPPPTVPGAVCPVPRVRSNNVPESLPPASMPYADHYSFTSPDRMNS 540
 Qy 670 SPYOPPPQGPVPPVPSGMAPVYDSRRIRWPPMYORDIITRSNLSLPPDMVMSVYQ 729
 Db 541 SPYOPPPQGPVPPVPSGMAPVYDSRRIRWPPMYORDIITRSNLSLPPDMVMSVYQ 600
 Db 730 TSLRERYNSLDGYYSYACQPSSEPRTTVPLREPCGHLKTSCEEQIRRKPDQWAQHTQK 789
 Db 601 TSLRERYNSLDGYYSYACQPSSEPRTTVPLREPCGHLKTSCEEQIRRKPDQWAQHTQK 660
 Qy 790 APLVSSLTPVATOSPTPPSPLESVDRADFSVSGTKFEDHLHSYPMSCGGTGSIN 849
 Db 661 APLVSSLTPVATOSPTPPSPLESVDRADFSVSGTKFEDHLHSYPMSCGGTGSIN 720
 Qy 850 AIDSEPKDVTANSNAVIMLDQSGDVKRVLHETORTRKEEPIITPSDGPIISKWGAIS 909
 Db 721 AIDSEPKDVTANSNAVIMLDQSGDVKRVLHETORTRKEEPIITPSDGPIISKWGAIS 780
 Qy 910 RSRTGHTTDVQATASQGATKPTISVSDVYPPVNAVDSSWSSYNEATSSAHYERDR 969
 Db 781 RSRTGHTTDVQATASQGATKPTISVSDVYPPVNAVDSSWSSYNEATSSAHYERDR 840
 Qy 970 FIVTDLSGRKHSSTGDLISLQOAKNSNLQORANALAMQKNSLDSGRHLTLNLL 1029
 Db 841 FIVTDLSGRKHSSTGDLISLQOAKNSNLQORANALAMQKNSLDSGRHLTLNLL 900
 Qy 1030 SKIELRNGELOSODYEDATDKPDRDIELETSALDTDEPDCOSEPTEEIIDIOLQGTSQ 1089
 Db 901 SKIELRNGELOSODYEDATDKPDRDIELETSALDTDEPDCOSEPIEEIIDLQGISSQ 960
 Qy 1090 NDQLINGMAVENGHPYQHQKEPPKOKKQSISGEDHVILEEQTKTILVTCSSQPLVIS 1149
 Db 961 NDQLINGMAVENGHPYQHQKEPPKOKKQSISGEDHVILEEQTKTILVTCSSQPLVIS 1020
 RESULT 13
 US-60-466-412-13598
 ; Sequence 13598, Application US/60466412
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01466
 ; CURRENT APPLICATION NUMBER: US/60/466,412
 ; CURRENT FILING DATE: 2003-04-30
 ; NUMBER OF SEQ ID NOS: 42941
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 13598
 ; LENGTH: 1062
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-466-412-13598
 Query Match 88.9%; Score 5525; DB 49; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1062; Conservative 0;
 Qy 130 MQRKLVTLLVNCOLVNEBEGVRAMRAARSGLGRTVTBLILQHQNQQLSALNLAVERGC 189
 Db 190 QFLGPWMQEAEALKVLLAEDGSLASLRKVLYLFWVORLERPFOASKTSIGHWVOLYRA 249
 Qy 611 QFLGPWMQEAEALKVLLAEDGSLASLRKVLYLFWVORLERPFOASKTSIGHWVOLYRA 120
 Db 250 SCKTKTRDESSSIMLKERSYEALREHDAQTWHAMEAGLTSBEQMSLULYGLA 309
 Db 121 SCFKVTKRDBDSLMLKEEFSRSYALRREHDAQVHIMAEAGLTSBEQMSLULYGLA 180
 Qy 310 HKSHMOSIDKUQSPSFAKSVQELTIVLQRTGDPANLNLRPHBLLANTDPNPAVSP 369
 Db 181 HKSHMOSIDKUQSPSFAKSVQELTIVLQRTGDPANLNLRPHBLLANTDPNPAVSP 240
 Qy 370 TWEQLENAMVAVKTVHGLDVTIONYSRKGHETPOPOPNSKXTSMCRDQGCGPRT 429
 Db 241 TWEQLENAMVAVKTVHGLDVTIONYSRKGHETPOPOPNSKXTSMCRDQGCGPRT 300
 Qy 430 NCTFAHSQEELEYKURNKKINATRTPELANKGVNTNTTAAVNIVSIGSTETGKI 489
 Db 301 NCTFAHSQEELEYKURNKKINATRTPELANKGVNTNTTAAVNIVSIGSTETGKI 360
 Qy 490 VPSTNGTISNAENSVSQSLISRSTDSTRLAETVKKGKVGANGQNAAGPSADSUTENKIGS 549
 Db 361 VPSTNGTISNAENSVSQSLISRSTDSTRLAETVKKGKVGANGQNAAGPSADSUTENKIGS 420
 Qy 550 PPKTPVSNAATTSAGSNVNGTELNSPKQSSPFLTRPVPPHSENIOYFQDPRTQIPFE 609
 Db 421 PPKTPVSNAATTSAGSNVNGTELNSPKQSSPFLTRPVPPHSENIOYFQDPRTQIPFE 480
 Qy 610 VPQYPTQGYPPPTVPGAVCPVPRVRSNNVPESLPPASMPYADHYSFTSPDRMNS 669
 Db 481 VPQYPTQGYPPPTVPGAVCPVPRVRSNNVPESLPPASMPYADHYSFTSPDRMNS 540
 Qy 670 SPYOPPPQGPVPPVPSGMAPVYDSRRIRWPPMYORDIITRSNLSLPPDMVMSVYQ 729
 Db 541 SPYOPPPQGPVPPVPSGMAPVYDSRRIRWPPMYORDIITRSNLSLPPDMVMSVYQ 600
 Db 730 TSLRERYNSLDGYYSYACQPSSEPRTTVPLREPCGHLKTSCEEQIRRKPDQWAQHTQK 789
 Db 601 TSLRERYNSLDGYYSYACQPSSEPRTTVPLREPCGHLKTSCEEQIRRKPDQWAQHTQK 660
 Qy 790 APLVSSLTPVATOSPTPPSPLESVDRADFSVSGTKFEDHLHSYPMSCGGTGSIN 849
 Db 661 APLVSSLTPVATOSPTPPSPLESVDRADFSVSGTKFEDHLHSYPMSCGGTGSIN 720
 Qy 850 AIDSEPKDVTANSNAVIMLDQSGDVKRVLHETORTRKEEPIITPSDGPIISKWGAIS 909
 Db 721 AIDSEPKDVTANSNAVIMLDQSGDVKRVLHETORTRKEEPIITPSDGPIISKWGAIS 780
 Qy 910 RSRTGHTTDVQATASQGATKPTISVSDVYPPVNAVDSSWSSYNEATSSAHYERDR 969
 Db 781 RSRTGHTTDVQATASQGATKPTISVSDVYPPVNAVDSSWSSYNEATSSAHYERDR 840
 Qy 970 FIVTDLSGRKHSSTGDLISLQOAKNSNLQORANALAMQKNSLDSGRHLTLNLL 1029
 Db 841 FIVTDLSGRKHSSTGDLISLQOAKNSNLQORANALAMQKNSLDSGRHLTLNLL 900
 Qy 1030 SKIELRNGELOSODYEDATDKPDRDIELETSALDTDEPDCOSEPIEEIIDLQGTSQ 1089
 Db 901 SKIELRNGELOSODYEDATDKPDRDIELETSALDTDEPDCOSEPIEEIIDLQGTSQ 960
 Qy 1090 NDQLINGMAVENGHPYQHQKEPPKOKKQSISGEDHVILEEQTKTILVTCSSQPLVIS 1149
 Db 961 NDQLINGMAVENGHPYQHQKEPPKOKKQSISGEDHVILEEQTKTILVTCSSQPLVIS 1020
 RESULT 14
 Query Match 88.9%; Score 5525; DB 49; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1062; Conservative 0;
 Qy 130 MQRKLVTLLVNCOLVNEBEGVRAMRAARSGLGRTVTBLILQHQNQQLSALNLAVERGC 189
 Db 190 QFLGPWMQEAEALKVLLAEDGSLASLRKVLYLFWVORLERPFOASKTSIGHWVOLYRA 249
 Db 611 QFLGPWMQEAEALKVLLAEDGSLASLRKVLYLFWVORLERPFOASKTSIGHWVOLYRA 120
 Qy 250 SCKTKTRDESSSIMLKERSYEALREHDAQTWHAMEAGLTSBEQMSLULYGLA 309
 Db 121 SCFKVTKRDBDSLMLKEEFSRSYALRREHDAQVHIMAEAGLTSBEQMSLULYGLA 180
 Qy 310 HKSHMOSIDKUQSPSFAKSVQELTIVLQRTGDPANLNLRPHBLLANTDPNPAVSP 369
 Db 181 HKSHMOSIDKUQSPSFAKSVQELTIVLQRTGDPANLNLRPHBLLANTDPNPAVSP 240
 Qy 370 TWEQLENAMVAVKTVHGLDVTIONYSRKGHETPOPOPNSKXTSMCRDQGCGPRT 429
 Db 241 TWEQLENAMVAVKTVHGLDVTIONYSRKGHETPOPOPNSKXTSMCRDQGCGPRT 300
 Qy 430 NCTFAHSQEELEYKURNKKINATRTPELANKGVNTNTTAAVNIVSIGSTETGKI 489
 Db 301 NCTFAHSQEELEYKURNKKINATRTPELANKGVNTNTTAAVNIVSIGSTETGKI 360
 Qy 490 VPSTNGTISNAENSVSQSLISRSTDSTRLAETVKKGKVGANGQNAAGPSADSUTENKIGS 549
 Db 361 VPSTNGTISNAENSVSQSLISRSTDSTRLAETVKKGKVGANGQNAAGPSADSUTENKIGS 420
 Qy 550 PPKTPVSNAATTSAGSNVNGTELNSPKQSSPFLTRPVPPHSENIOYFQDPRTQIPFE 609
 Db 421 PPKTPVSNAATTSAGSNVNGTELNSPKQSSPFLTRPVPPHSENIOYFQDPRTQIPFE 480
 Qy 610 VPQYPTQGYPPPTVPGAVCPVPRVRSNNVPESLPPASMPYADHYSFTSPDRMNS 669
 Db 481 VPQYPTQGYPPPTVPGAVCPVPRVRSNNVPESLPPASMPYADHYSFTSPDRMNS 540
 Qy 670 SPYOPPPQGPVPPVPSGMAPVYDSRRIRWPPMYORDIITRSNLSLPPDMVMSVYQ 729
 Db 541 SPYOPPPQGPVPPVPSGMAPVYDSRRIRWPPMYORDIITRSNLSLPPDMVMSVYQ 600
 Db 730 TSLRERYNSLDGYYSYACQPSSEPRTTVPLREPCGHLKTSCEEQIRRKPDQWAQHTQK 789
 Db 601 TSLRERYNSLDGYYSYACQPSSEPRTTVPLREPCGHLKTSCEEQIRRKPDQWAQHTQK 660
 Qy 790 APLVSSLTPVATOSPTPPSPLESVDRADFSVSGTKFEDHLHSYPMSCGGTGSIN 849
 Db 661 APLVSSLTPVATOSPTPPSPLESVDRADFSVSGTKFEDHLHSYPMSCGGTGSIN 720
 Qy 850 AIDSEPKDVTANSNAVIMLDQSGDVKRVLHETORTRKEEPIITPSDGPIISKWGAIS 909
 Db 721 AIDSEPKDVTANSNAVIMLDQSGDVKRVLHETORTRKEEPIITPSDGPIISKWGAIS 780
 Qy 910 RSRTGHTTDVQATASQGATKPTISVSDVYPPVNAVDSSWSSYNEATSSAHYERDR 969
 Db 781 RSRTGHTTDVQATASQGATKPTISVSDVYPPVNAVDSSWSSYNEATSSAHYERDR 840
 Qy 970 FIVTDLSGRKHSSTGDLISLQOAKNSNLQORANALAMQKNSLDSGRHLTLNLL 1029
 Db 841 FIVTDLSGRKHSSTGDLISLQOAKNSNLQORANALAMQKNSLDSGRHLTLNLL 900
 Qy 1030 SKIELRNGELOSODYEDATDKPDRDIELETSALDTDEPDCOSEPIEEIIDLQGTSQ 1089
 Db 901 SKIELRNGELOSODYEDATDKPDRDIELETSALDTDEPDCOSEPIEEIIDLQGTSQ 960
 Qy 1090 NDQLINGMAVENGHPYQHQKEPPKOKKQSISGEDHVILEEQTKTILVTCSSQPLVIS 1149
 Db 961 NDQLINGMAVENGHPYQHQKEPPKOKKQSISGEDHVILEEQTKTILVTCSSQPLVIS 1020
 RESULT 14
 US-10-485-225-8

; Sequence 8, Application US/10485225
; GENERAL INFORMATION:
; APPLICANT: Greener, Tsvika
; APPLICANT: Moskowitz, Haim
; APPLICANT: Reiss, Yuval
; APPLICANT: Alroy, Itai
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; MODULATION OF VIRAL MATURATION
; FILE REFERENCE: PROL-P02-001
; CURRENT APPLICATION NUMBER: US/10/485, 225
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/308, 958
; PRIOR FILING DATE: 2001-07-31
; PRIORITY NUMBER: US 60/345, 846
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 1048
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-485-225-8

Query Match 88.2%; Score 5483; DB 34; Length 1048;
Best Local Similarity 100.0%; Pred. No: 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1048; Conservative 0;

Qy 1 MPVQAAQWTSPLSCPYCNEFDENVHKPISIGCSHFTVKCLNKUHRKCPFPDQTAINTD 60
Db 1 MPVQAAQWTSPLSCPYCNEFDENVHKPISIGCSHFTVKCLNKUHRKCPFPDQTAINTD 60
Qy 61 IDVLPUNFALLQVAGQVPHOSIKLSNIGKHKHEVAKCVEDALYKPLSGKGVAS 120
Db 61 IDVLPUNFALLQVAGQVPHOSIKLSNIGKHKHEVAKCVEDALYKPLSGKGVAS 120
Qy 121 LNQSAISRPMOKLVLINCOLVEEGRVRAMRAARSGLERTVTELQLOKONPOQLANL 180
Db 121 LNQSAISRPMOKLVLINCOLVEEGRVRAMRAARSGLERTVTELQLOKONPOQLANL 180
Qy 181 WAAVRARGCOFLGPAMQBEALKVILALEDGSALSRSKVLVFVWRLEPRPPQASKTIG 240
Db 181 WAAVRARGCOFLGPAMQBEALKVILALEDGSALSRSKVLVFVWRLEPRPPQASKTIG 240
Qy 241 HWVQOLYRASCFCFKVTRDESSLMOLKEERSYEARREDAQVHIMERGLRISPEOW 300
Db 241 HWVQOLYRASCFCFKVTRDESSLMOLKEERSYEARREDAQVHIMERGLRISPEOW 300
Qy 301 SSIJKDLAKSHMSIIDLQKQSPESFAKSQVELTIVLQRTGDPANLNRLRPHELLANI 360
Db 301 SSIJKDLAKSHMSIIDLQKQSPESFAKSQVELTIVLQRTGDPANLNRLRPHELLANI 360
Qy 361 DPNDPAVSPTWEQLENAMVAVYKTVVHLVDSTIQTNSRKGHETQPQPNNSKVKTCRDLR 420
Db 361 DPNDPAVSPTWEQLENAMVAVYKTVVHLVDSTIQTNSRKGHETQPQPNNSKVKTCRDLR 420
Qy 421 QGGCPRGTNTCAQSQELLYKRLNKKTATVTPPLANKVGVNNTVTAGNIVSI 480
Db 421 QGGCPRGTNTCAQSQELLYKRLNKKTATVTPPLANKVGVNNTVTAGNIVSI 480
Qy 481 GSTETGKIKPSTINGSNAENSVSQSLRSRSTIRALETKVKGANGQNAAGPSAD 540
Db 481 GSTETGKIKPSTINGSNAENSVSQSLRSRSTIRALETKVKGANGQNAAGPSAD 540
Qy 541 SVTENKIGSPRTPVNSVVAATSAGPNSVNGTELNVSFIQKSSPFLTRPVVYPPHSENQYFQ 600
Db 541 SVTENKIGSPRTPVNSVVAATSAGPNSVNGTELNVSFIQKSSPFLTRPVVYPPHSENQYFQ 600
Qy 541 SVTENKIGSPRTPVNSVVAATSAGPNSVNGTELNVSFIQKSSPFLTRPVVYPPHSENQYFQ 600
Db 601 DFRTOIPFPEVQYPOGYYPPEPTVAGVACVCPVFRVRSNNVPESSLPPASMPYADHYST 660
Db 601 DFRTOIPFPEVQYPOGYYPPEPTVAGVACVCPVFRVRSNNVPESSLPPASMPYADHYST 660
Qy 661 FSPRDNMSSPQPPQPKYPPVPPSGMAPVDSRRTMPYMDITRSLPPM 720
; US-10-485-225-8

Query Match 71.1%; Score 4416; DB 24; Length 869;
Best Local Similarity 99.8%; Pred. No: 0; Mismatches 0; Indels 0; Gaps 0;
Matches 844; Conservative 2;

Qy 781 OWAQHFTQKAPLVSSTLPVATQSPTPSPFLSVDRADFEBSVSGTKFEEDHLSHYSWWS 840
Db 781 OWAQHFTQKAPLVSSTLPVATQSPTPSPFLSVDRADFEBSVSGTKFEEDHLSHYSWWS 840
Qy 841 CGTICSCINAIDSEPKDVIANSNAYLMDLUSGDVKKRVRHFETOARTKEDPITIPSDGP 900
Db 841 CGTICSCINAIDSEPKDVIANSNAYLMDLUSGDVKKRVRHFETOARTKEDPITIPSDGP 900
Qy 901 IISKNGAISISSRSRTGHTTPVOATASQGATKPSVSYVWPMWMSYGEATS 960
Db 901 IISKNGAISISSRSRTGHTTPVOATASQGATKPSVSYVWPMWMSYGEATS 960
Qy 961 SAHYVERDRFTVTDLSGHKRHSSTGDLSSLQAKNSNLLQREANALAMQKONSLDE 1020
Db 961 SAHYVERDRFTVTDLSGHKRHSSTGDLSSLQAKNSNLLQREANALAMQKONSLDE 1020
Qy 1021 GRHLTNLNLSKEIELRNLNGELQSDYTEDA 1048
Db 1021 GRHLTNLNLSKEIELRNLNGELQSDYTEDA 1048

RESULT 15
US-09-488-725A-3-499
Sequence 3499, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784F1PCT
CURRENT APPLICATION NUMBER: US/09/488, 725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488, 725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/09/552, 317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US/09/598, 042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/620, 312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US/09/653, 450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US/09/662, 191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US/09/693, 036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US/09/727, 344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: Pt_Fl_Genes_b Versions 1.0
SEQ ID NO: 3499
LENGTH: 870
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-3499

Query Match 71.1%; Score 4416; DB 24; Length 869;
Best Local Similarity 99.8%; Pred. No: 0; Mismatches 0; Indels 0; Gaps 0;
Matches 844; Conservative 2;

Qy 196 MOBEALKVLVLALEDGSALSRSKVLVFVWRLEPRPPQASKTIGHVQOLYRASCFCVT 255
Db 1 MOBEALKVLVLALEDGSALSRSKVLVFVWRLEPRPPQASKTIGHVQOLYRASCFCVT 255
Qy 256 KRDDESSLMOLKEERSYEARREDAQVHIMERGLRISPEOWSSLVYCDLAHKSMQ 315
Db 61 KRDDESSLMOLKEERSYEARREDAQVHIMERGLRISPEOWSSLVYCDLAHKSMQ 315
Qy 316 SIIDKLQSPESFAKSQVELTIVLQRTGDPANLNRLRPHELLANI DPNDPAVSPTWEQLE 375

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Db          ||||||| 121 SITDKLQSPFSAKSVQBLTIVLQRGFDPAINLRPHSELANTIDPNPDAVSPTWOLE 180
QY          ||||||| 376 NAMVAVKTVVFLGLVDRIONTSRKGHTQPQOPNPKYTKSMCRDURQGGPPRGNTCTFAH 435
Db          ||||||| 181 NAMVAVKTVVFLGLVDRIONTSRKGHTQPQOPNPKYTKSMCRDURQGGPPRGNTCTFAH 240
QY          ||||||| 436 SOEELKXRLANKKINATVRTEPLINKVGVNNTVTAGNVISVIGSTETTGKVIPSTNG 495
Db          ||||||| 241 SOEELKXRLANKKINATVRTEPLINKVGVNNTVTAGNVISVIGSTETTGKVIPSTNG 300
Qy          ||||||| 496 ISNAENSVSLRSRSDTSLRALETTKKVGKGANGONAGPSASVTEENIGSPPKTPV 555
Db          ||||||| 301 ISNAENSVSLRSRSDTSLRALETTKKVGKGANGONAGPSASVTEENIGSPPKTPV 360
Qy          ||||||| 556 SVAATSAGSPNGVTELNSPQKSSPLTRPVYPPHSENIQFQDPRTOIPEPQYQ 615
Db          ||||||| 361 SVAATSAGSPNGVTELNSPQKSSPLTRPVYPPHSENIQFQDPRTOIPEPQYQ 420
Qy          ||||||| 616 TGYYPDPPTVAGVACVPRFRWSNNVPESSLPPASMPYADHYSFSPRDRMNSSPYQPP 675
Db          ||||||| 421 TGYYPDPPTVAGVACVPRFRWSNNVPESSLPPASMPYADHYSFSPRDRMNSSPYQPP 480
Qy          ||||||| 676 PRQPYGRVPPVPSGMATPVYSSRIRRPMQCDDTIRSNLIPPMOMHSSVYQTSRLER 735
Db          ||||||| 481 PRQPYGRVPPVPSGMATPVYSSRIRRPMQCDDTIRSNLIPPMOMHSSVYQTSRLER 540
Qy          ||||||| 736 YNSLDGTYSVACQPPSPRTVPLPBPCHNIKTSCEQIRKPQDWAQHPTQAKLYSS 795
Db          ||||||| 541 YNSLDGTYSVACQPPSPRTVPLPBPCHNIKTSCEQIRKPQDWAQHPTQAKLYSS 600
Db          ||||||| 541 YNSLDGTYSVACQPPSPRTVPLPBPCHNIKTSCEQIRKPQDWAQHPTQAKLYSS 600
Db          ||||||| 796 TLPVATOSPTPSPLFSVDRADFSESVSGTKFEEDHLHSYSPWSCGTIGSCINAIDSEP 855
Db          ||||||| 601 TLPVATOSPTPSPLFSVDRADFSESVSGTKFEEDHLHSYSPWSCGTIGSCINAIDSEP 660
Qy          ||||||| 856 KDVIANSNAVLMDSDGDKVRVHLFETQRTKEEDPITPSDGPI1SKWGAISRSRTG 915
Db          ||||||| 661 KDVIANSNAVLMDSDGDKVRVHLFETQRTKEEDPITPSDGPI1SKWGAISRSRTG 720
Qy          ||||||| 916 YHTTDPVQATASQGSAKPKISYDVPYVNAUDSRSSYGHATSAHYVERDRFTDL 975
Db          ||||||| 721 YHTTDPVQATASQGSAKPKISYDVPYVNAUDSRSSYGHATSAHYVERDRFTDL 780
Db          ||||||| 976 SGHRKHSSTGDLSELQAKNSLLQREANALAMQKWNLSDEGRHLTLNLSSKEIEL 1035
Db          ||||||| 781 SGHRKHSSTGDLSELQAKNSLLQREANALAMQKWNLSDEGRHLTLNLSSKEIEL 840
Qy          ||||||| 1036 RNGELQ 1041
Db          ||||||| 841 RNGEVK 846

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Search completed: May 24, 2006, 12:54:40
 Job time : 301 secs